



SEQUENCE LISTING

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TECH CENTER 1600/2800

(1) GENERAL INFORMATION:

(i) APPLICANT: ALBERTSEN, HANS
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(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: [102] 154

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

((vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/442,489
(B) FILING DATE: 18-NOV-1999
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/452,654
(B) FILING DATE: 25-MAY-1995

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,548
(B) FILING DATE: 12-AUG-1994

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/741,940
(B) FILING DATE: 08-AUG-1001

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A.
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(C) REFERENCE/DOCKET NUMBER: 1107.035574

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5 (APC)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 34..8562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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| GGACTCGGAA ATGAGGTCCA AGGGTAGCCA AGG ATG GCT GCA GCT TCA TAT GAT | 54 |
| Met Ala Ala Ala Ser Tyr Asp | |
| 1 5 | |
| CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT | 102 |
| Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu | |
| 10 15 20 | |
| CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT | 150 |
| Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr | |
| 25 30 35 | |
| GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT | 198 |
| Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile | |

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|---|--|-----|--|-----|--|-----|-----|
| 40 | | 45 | | 50 | | 55 | |
| GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT | | | | | | | 246 |
| Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg | | | | | | | |
| | | 60 | | 65 | | 70 | |
| CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG | | | | | | | 294 |
| Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu | | | | | | | |
| | | 75 | | 80 | | 85 | |
| CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA | | | | | | | 342 |
| Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val | | | | | | | |
| | | 90 | | 95 | | 100 | |
| TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA | | | | | | | 390 |
| Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro | | | | | | | |
| | | 105 | | 110 | | 115 | |
| AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGA TAT TTA GAA | | | | | | | 438 |
| Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu | | | | | | | |
| | | 120 | | 125 | | 130 | 135 |
| GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA | | | | | | | 486 |
| Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu | | | | | | | |
| | | 140 | | 145 | | 150 | |
| GAA AAG GAA AAA GAC TGG TAT TAC GCT CAA CTT CAG AAT CTC ACT AAA | | | | | | | 534 |
| Glu Lys Glu Lys Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr Lys | | | | | | | |
| | | 155 | | 160 | | 165 | |
| AGA ATA GAT AGT CTT CCT TTA ACT GAA AAT TTT TCC TTA CAA ACA GAT | | | | | | | 582 |
| Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp | | | | | | | |
| | | 170 | | 175 | | 180 | |
| TTG ACC AGA AGG CAA TTG GAA TAT GAA GCA AGG CAA ATC AGA GTT GCG | | | | | | | 630 |
| Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala | | | | | | | |
| | | 185 | | 190 | | 195 | |
| ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG | | | | | | | 678 |
| Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln | | | | | | | |
| | | 200 | | 205 | | 210 | 215 |
| CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA | | | | | | | 726 |
| Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile | | | | | | | |
| | | 220 | | 225 | | 230 | |
| CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG | | | | | | | 774 |
| Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln | | | | | | | |
| | | 235 | | 240 | | 245 | |
| AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT | | | | | | | 822 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asn | Lys | His | Glu | Thr | Gly | Ser | His | Asp | Ala | Glu | Arg | Gln | Asn | Glu | Gly | |
| | | 250 | | | | | 255 | | | | | 260 | | | | |
| CAA | GGA | GTG | GGA | GAA | ATC | AAC | ATG | GCA | ACT | TCT | GGT | AAT | GGT | CAG | GGT | 870 |
| Gln | Gly | Val | Gly | Glu | Ile | Asn | Met | Ala | Thr | Ser | Gly | Asn | Gly | Gln | Gly | |
| | 265 | | | | | 270 | | | | | 275 | | | | | |
| TCA | ACT | ACA | CGA | ATG | GAC | CAT | GAA | ACA | GCC | AGT | GTT | TTG | AGT | TCT | AGT | 918 |
| Ser | Thr | Thr | Arg | Met | Asp | His | Glu | Thr | Ala | Ser | Val | Leu | Ser | Ser | Ser | |
| 280 | | | | | 285 | | | | | 290 | | | | | 295 | |
| AGC | ACA | CAC | TCT | GCA | CCT | CGA | AGG | CTG | ACA | AGT | CAT | CTG | GGA | ACC | AAG | 966 |
| Ser | Thr | His | Ser | Ala | Pro | Arg | Arg | Leu | Thr | Ser | His | Leu | Gly | Thr | Lys | |
| | | | | 300 | | | | | 305 | | | | | 310 | | |
| GTG | GAA | ATG | GTG | TAT | TCA | TTG | TTG | TCA | ATG | CTT | GGT | ACT | CAT | GAT | AAG | 1014 |
| Val | Glu | Met | Val | Tyr | Ser | Leu | Leu | Ser | Met | Leu | Gly | Thr | His | Asp | Lys | |
| | | | 315 | | | | | 320 | | | | | 325 | | | |
| GAT | GAT | ATG | TCG | CGA | ACT | TTG | CTA | GCT | ATG | TCT | AGC | TCC | CAA | GAC | AGC | 1062 |
| Asp | Asp | Met | Ser | Arg | Thr | Leu | Leu | Ala | Met | Ser | Ser | Ser | Gln | Asp | Ser | |
| | | 330 | | | | | 335 | | | | | 340 | | | | |
| TGT | ATA | TCC | ATG | CGA | CAG | TCT | GGA | TGT | CTT | CCT | CTC | CTC | ATC | CAG | CTT | 1110 |
| Cys | Ile | Ser | Met | Arg | Gln | Ser | Gly | Cys | Leu | Pro | Leu | Leu | Ile | Gln | Leu | |
| | 345 | | | | | 350 | | | | | 355 | | | | | |
| TTA | CAT | GGC | AAT | GAC | AAA | GAC | TCT | GTA | TTG | TTG | GGA | AAT | TCC | CGG | GGC | 1158 |
| Leu | His | Gly | Asn | Asp | Lys | Asp | Ser | Val | Leu | Leu | Gly | Asn | Ser | Arg | Gly | |
| 360 | | | | | 365 | | | | 370 | | | | | | 375 | |
| AGT | AAA | GAG | GCT | CGG | GCC | AGG | GCC | AGT | GCA | GCA | CTC | CAC | AAC | ATC | ATT | 1206 |
| Ser | Lys | Glu | Ala | Arg | Ala | Arg | Ala | Ser | Ala | Ala | Leu | His | Asn | Ile | Ile | |
| | | | | 380 | | | | | 385 | | | | | 390 | | |
| CAC | TCA | CAG | CCT | GAT | GAC | AAG | AGA | GGC | AGG | CGT | GAA | ATC | CGA | GTC | CTT | 1254 |
| His | Ser | Gln | Pro | Asp | Asp | Lys | Arg | Gly | Arg | Arg | Glu | Ile | Arg | Val | Leu | |
| | | | 395 | | | | | 400 | | | | | 405 | | | |
| CAT | CTT | TTG | GAA | CAG | ATA | CGC | GCT | TAC | TGT | GAA | ACC | TGT | TGG | GAG | TGG | 1302 |
| His | Leu | Leu | Glu | Gln | Ile | Arg | Ala | Tyr | Cys | Glu | Thr | Cys | Trp | Glu | Trp | |
| | | 410 | | | | | 415 | | | | | 420 | | | | |
| CAG | GAA | GCT | CAT | GAA | CCA | GGC | ATG | GAC | CAG | GAC | AAA | AAT | CCA | ATG | CCA | 1350 |
| Gln | Glu | Ala | His | Glu | Pro | Gly | Met | Asp | Gln | Asp | Lys | Asn | Pro | Met | Pro | |
| | 425 | | | | | 430 | | | | | 435 | | | | | |
| GCT | CCT | GTT | GAA | CAT | CAG | ATC | TGT | CCT | GCT | GTG | TGT | GTT | CTA | ATG | AAA | 1398 |
| Ala | Pro | Val | Glu | His | Gln | Ile | Cys | Pro | Ala | Val | Cys | Val | Leu | Met | Lys | |
| 440 | | | | | 445 | | | | | 450 | | | | | 455 | |

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| CTT TCA TTT GAT GAA GAG CAT AGA CAT GCA ATG AAT GAA CTA GGG GGA Leu Ser Phe Asp Glu Glu His Arg His Ala Met Asn Glu Leu Gly Gly 460 465 470 | 1446 |
| CTA CAG GCC ATT GCA GAA TTA TTG CAA GTG GAC TGT GAA ATG TAT GGG Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp Cys Glu Met Tyr Gly 475 480 485 | 1494 |
| CTT ACT AAT GAC CAC TAC AGT ATT ACA CTA AGA CGA TAT GCT GGA ATG Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg Arg Tyr Ala Gly Met 490 495 500 | 1542 |
| GCT TTG ACA AAC TTG ACT TTT GGA GAT GTA GCC AAC AAG GCT ACG CTA Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala Asn Lys Ala Thr Leu 505 510 515 | 1590 |
| TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser 520 525 530 535 | 1638 |
| GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu 540 545 550 | 1686 |
| TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly 555 560 565 | 1734 |
| AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser 570 575 580 | 1782 |
| ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG AAT TTG TCA GCA CAT TGC Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys 585 590 595 | 1830 |
| ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe 600 605 610 615 | 1878 |
| TTG GTT GGC ACT CTT ACT TAC CGG AGC CAG ACA AAC ACT TTA GCC ATT Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile 620 625 630 | 1926 |
| ATT GAA AGT GGA GGT GGG ATA TTA CGG AAT GTG TCC AGC TTG ATA GCT Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala 635 640 645 | 1974 |
| ACA AAT GAG GAC CAC AGG CAA ATC CTA AGA GAG AAC AAC TGT CTA CAA Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln 650 655 660 | 2022 |

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| ACT TTA TTA CAA CAC TTA AAA TCT CAT AGT TTG ACA ATA GTC AGT AAT Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn 665 670 675 | 2070 |
| GCA TGT GGA ACT TTG TGG AAT CTC TCA GCA AGA AAT CCT AAA GAC CAG Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln 680 685 690 695 | 2118 |
| GAA GCA TTA TGG GAC ATG GGG GCA GTT AGC ATG CTC AAG AAC CTC ATT Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile 700 705 710 | 2166 |
| CAT TCA AAG CAC AAA ATG ATT GCT ATG GGA AGT GCT GCA GCT TTA AGG His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg 715 720 725 | 2214 |
| AAT CTC ATG GCA AAT AGG CCT GCG AAG TAC AAG GAT GCC AAT ATT ATG Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met 730 735 740 | 2262 |
| TCT CCT GGC TCA AGC TTG CCA TCT CTT CAT GTT AGG AAA CAA AAA GCC Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala 745 750 755 | 2310 |
| CTA GAA GCA GAA TTA GAT GCT CAG CAC TTA TCA GAA ACT TTT GAC AAT Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn 760 765 770 775 | 2358 |
| ATA GAC AAT TTA AGT CCC AAG GCA TCT CAT CGT AGT AAG CAG AGA CAC Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His 780 785 790 | 2406 |
| AAG CAA AGT CTC TAT GGT GAT TAT GTT TTT GAC ACC AAT CGA CAT GAT Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp 795 800 805 | 2454 |
| GAT AAT AGG TCA GAC AAT TTT AAT ACT GGC AAC ATG ACT GTC CTT TCA Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser 810 815 820 | 2502 |
| CCA TAT TTG AAT ACT ACA GTG TTA CCC AGC TCC TCT TCA TCA AGA GGA Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Arg Gly 825 830 835 | 2550 |
| AGC TTA GAT AGT TCT CGT TCT GAA AAA GAT AGA AGT TTG GAG AGA GAA Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg Ser Leu Glu Arg Glu 840 845 850 855 | 2598 |

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| CGC GGA ATT GGT CTA GGC AAC TAC CAT CCA GCA ACA GAA AAT CCA GGA Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly 860 865 870 | 2646 |
| ACT TCT TCA AAG CGA GGT TTG CAG ATC TCC ACC ACT GCA GCC CAG ATT Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile 875 880 885 | 2694 |
| GCC AAA GTC ATG GAA GAA GTG TCA GCC ATT CAT ACC TCT CAG GAA GAC Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp 890 895 900 | 2742 |
| AGA AGT TCT GGG TCT ACC ACT GAA TTA CAT TGT GTG ACA GAT GAG AGA Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg 905 910 915 | 2790 |
| AAT GCA CTT AGA AGA AGC TCT GCT GCC CAT ACA CAT TCA AAC ACT TAC Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr 920 925 930 935 | 2838 |
| AAT TTC ACT AAG TCG GAA AAT TCA AAT AGG ACA TGT TCT ATG CCT TAT Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr Cys Ser Met Pro Tyr 940 945 950 | 2886 |
| GCC AAA TTA GAA TAC AAG AGA TCT TCA AAT GAT AGT TTA AAT AGT GTC Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp Ser Leu Asn Ser Val 955 960 965 | 2934 |
| AGT AGT AAT GAT GGT TAT GGT AAA AGA GGT CAA ATG AAA CCC TCG ATT Ser Ser Asn Asp Gly Tyr Gly Lys Arg Gly Gln Met Lys Pro Ser Ile 970 975 980 | 2982 |
| GAA TCC TAT TCT GAA GAT GAT GAA AGT AAG TTT TGC AGT TAT GGT CAA Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe Cys Ser Tyr Gly Gln 985 990 995 | 3030 |
| TAC CCA GCC GAC CTA GCC CAT AAA ATA CAT AGT GCA AAT CAT ATG GAT Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser Ala Asn His Met Asp 1000 1005 1010 1015 | 3078 |
| GAT AAT GAT GGA GAA CTA GAT ACA CCA ATA AAT TAT AGT CTT AAA TAT Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn Tyr Ser Leu Lys Tyr 1020 1025 1030 | 3126 |
| TCA GAT GAG CAG TTG AAC TCT GGA AGG CAA AGT CCT TCA CAG AAT GAA Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln Ser Pro Ser Gln Asn Glu 1035 1040 1045 | 3174 |
| AGA TGG GCA AGA CCC AAA CAC ATA ATA GAA GAT GAA ATA AAA CAA AGT Arg Trp Ala Arg Pro Lys His Ile Ile Glu Asp Glu Ile Lys Gln Ser 1050 1055 1060 | 3222 |

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| GAG CAA AGA CAA TCA AGG AAT CAA AGT ACA ACT TAT CCT GTT TAT ACT Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr Thr Tyr Pro Val Tyr Thr 1065 1070 1075 | 3270 |
| GAG AGC ACT GAT GAT AAA CAC CTC AAG TTC CAA CCA CAT TTT GGA CAG Glu Ser Thr Asp Asp Lys His Leu Lys Phe Gln Pro His Phe Gly Gln 1080 1085 1090 1095 | 3318 |
| CAG GAA TGT GTT TCT CCA TAC AGG TCA CGG GGA GCC AAT GGT TCA GAA Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg Gly Ala Asn Gly Ser Glu 1100 1105 1110 | 3366 |
| ACA AAT CGA GTG GGT TCT AAT CAT GGA ATT AAT CAA AAT GTA AGC CAG Thr Asn Arg Val Gly Ser Asn His Gly Ile Asn Gln Asn Val Ser Gln 1115 1120 1125 | 3414 |
| TCT TTG TGT CAA GAA GAT GAC TAT GAA GAT GAT AAG CCT ACC AAT TAT Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp Asp Lys Pro Thr Asn Tyr 1130 1135 1140 | 3462 |
| AGT GAA CGT TAC TCT GAA GAA GAA CAG CAT GAA GAA GAA GAG AGA CCA Ser Glu Arg Tyr Ser Glu Glu Glu Gln His Glu Glu Glu Glu Arg Pro 1145 1150 1155 | 3510 |
| ACA AAT TAT AGC ATA AAA TAT AAT GAA GAG AAA CGT CAT GTG GAT CAG Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu Lys Arg His Val Asp Gln 1160 1165 1170 1175 | 3558 |
| CCT ATT GAT TAT AGT TTA AAA TAT GCC ACA GAT ATT CCT TCA TCA CAG Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr Asp Ile Pro Ser Ser Gln 1180 1185 1190 | 3606 |
| AAA CAG TCA TTT TCA TTC TCA AAG AGT TCA TCT GGA CAA AGC AGT AAA Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser Gly Gln Ser Ser Lys 1195 1200 1205 | 3654 |
| ACC GAA CAT ATG TCT TCA AGC AGT GAG AAT ACG TCC ACA CCT TCA TCT Thr Glu His Met Ser Ser Ser Ser Glu Asn Thr Ser Thr Pro Ser Ser 1210 1215 1220 | 3702 |
| AAT GCC AAG AGG CAG AAT CAG CTC CAT CCA AGT TCT GCA CAG AGT AGA Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg 1225 1230 1235 | 3750 |
| AGT GGT CAG CCT CAA AAG GCT GCC ACT TGC AAA GTT TCT TCT ATT AAC Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn 1240 1245 1250 1255 | 3798 |

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| CAA GAA ACA ATA CAG ACT TAT TGT GTA GAA GAT ACT CCA ATA TGT TTT Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe 1260 1265 1270 | 3846 |
| TCA AGA TGT AGT TCA TTA TCA TCT TTG TCA TCA GCT GAA GAT GAA ATA Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile 1275 1280 1285 | 3894 |
| GGA TGT AAT CAG ACG ACA CAG GAA GCA GAT TCT GCT AAT ACC CTG CAA Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln 1290 1295 1300 | 3942 |
| ATA GCA GAA ATA AAA GGA AAG ATT GGA ACT AGG TCA GCT GAA GAT CCT Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro 1305 1310 1315 | 3990 |
| GTG AGC GAA GTT CCA GCA GTG TCA CAG CAC CCT AGA ACC AAA TCC AGC Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser 1320 1325 1330 1335 | 4038 |
| AGA CTG CAG GGT TCT AGT TTA TCT TCA GAA TCA GCC AGG CAC AAA GCT Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala 1340 1345 1350 | 4086 |
| GTT GAA TTT CCT TCA GGA GCG AAA TCT CCC TCC AAA AGT GGT GCT CAG Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln 1355 1360 1365 | 4134 |
| ACA CCC AAA AGT CCA CCT GAA CAC TAT GTT CAG GAG ACC CCA CTC ATG Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met 1370 1375 1380 | 4182 |
| TTT AGC AGA TGT ACT TCT GTC AGT TCA CTT GAT AGT TTT GAG AGT CGT Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg 1385 1390 1395 | 4230 |
| TCG ATT GCC AGC TCC GTT CAG AGT GAA CCA TGC AGT GGA ATG GTA AGT Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser 1400 1405 1410 1415 | 4278 |
| GGC ATT ATA AGC CCC AGT GAT CTT CCA GAT AGC CCT GGA CAA ACC ATG Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met 1420 1425 1430 | 4326 |
| CCA CCA AGC AGA AGT AAA ACA CCT CCA CCA CCT CCT CAA ACA GCT CAA Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Pro Gln Thr Ala Gln 1435 1440 1445 | 4374 |
| ACC AAG CGA GAA GTA CCT AAA AAT AAA GCA CCT ACT GCT GAA AAG AGA Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg 1450 1455 1460 | 4422 |

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| GAG AGT GGA CCT AAG CAA GCT GCA GTA AAT GCT GCA GTT CAG AGG GTC Glu Ser Gly Pro Lys Gln Ala Ala Val Asn Ala Ala Val Gln Arg Val 1465 1470 1475 | 4470 |
| CAG GTT CTT CCA GAT GCT GAT ACT TTA TTA CAT TTT GCC ACA GAA AGT Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser 1480 1485 1490 1495 | 4518 |
| ACT CCA GAT GGA TTT TCT TGT TCA TCC AGC CTG AGT GCT CTG AGC CTC Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Leu Ser Ala Leu Ser Leu 1500 1505 1510 | 4566 |
| GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA Asp Glu Pro Phe Ile Gln Lys Asp Val Glu Leu Arg Ile Met Pro Pro 1515 1520 1525 | 4614 |
| GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys 1530 1535 1540 | 4662 |
| GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser 1545 1550 1555 | 4710 |
| GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT GAT ATT GAA ATA CTA Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Ile Glu Ile Leu 1560 1565 1570 1575 | 4758 |
| GAA GAA TGT ATT ATT TCT GCC ATG CCA ACA AAG TCA TCA CGT AAA GGC Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Gly 1580 1585 1590 | 4806 |
| AAA AAG CCA GCC CAG ACT GCT TCA AAA TTA CCT CCA CCT GTG GCA AGG Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu Pro Pro Pro Val Ala Arg 1595 1600 1605 | 4854 |
| AAA CCA AGT CAG CTG CCT GTG TAC AAA CTT CTA CCA TCA CAA AAC AGG Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Leu Pro Ser Gln Asn Arg 1610 1615 1620 | 4902 |
| TTG CAA CCC CAA AAG CAT GTT AGT TTT ACA CCG GGG GAT GAT ATG CCA Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro 1625 1630 1635 | 4950 |
| CGG GTG TAT TGT GTT GAA GGG ACA CCT ATA AAC TTT TCC ACA GCT ACA Arg Val Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr 1640 1645 1650 1655 | 4998 |

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| TCT CTA AGT GAT CTA ACA ATC GAA TCC CCT CCA AAT GAG TTA GCT GCT Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro Pro Asn Glu Leu Ala Ala 1660 1665 1670 | 5046 |
| GGA GAA GGA GTT AGA GGA GGA GCA CAG TCA GGT GAA TTT GAA AAA CGA Gly Glu Gly Val Arg Gly Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg 1675 1680 1685 | 5094 |
| GAT ACC ATT CCT ACA GAA GGC AGA AGT ACA GAT GAG GCT CAA GGA GGA Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly 1690 1695 1700 | 5142 |
| AAA ACC TCA TCT GTA ACC ATA CCT GAA TTG GAT GAC AAT AAA GCA GAG Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu 1705 1710 1715 | 5190 |
| GAA GGT GAT ATT CTT GCA GAA TGC ATT AAT TCT GCT ATG CCC AAA GGG Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn Ser Ala Met Pro Lys Gly 1720 1725 1730 1735 | 5238 |
| AAA AGT CAC AAG CCT TTC CGT GTG AAA AAG ATA ATG GAC CAG GTC CAG Lys Ser His Lys Pro Phe Arg Val Lys Lys Ile Met Asp Gln Val Gln 1740 1745 1750 | 5286 |
| CAA GCA TCT GCG TCG TCT TCT GCA CCC AAC AAA AAT CAG TTA GAT GGT Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn Lys Asn Gln Leu Asp Gly 1755 1760 1765 | 5334 |
| AAG AAA AAG AAA CCA ACT TCA CCA GTA AAA CCT ATA CCA CAA AAT ACT Lys Lys Lys Lys Pro Thr Ser Pro Val Lys Pro Ile Pro Gln Asn Thr 1770 1775 1780 | 5382 |
| GAA TAT AGG ACA CGT GTA AGA AAA AAT GCA GAC TCA AAA AAT AAT TTA Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu 1785 1790 1795 | 5430 |
| AAT GCT GAG AGA GTT TTC TCA GAC AAC AAA GAT TCA AAG AAA CAG AAT Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn 1800 1805 1810 1815 | 5478 |
| TTG AAA AAT AAT TCC AAG GAC TTC AAT GAT AAG CTC CCA AAT AAT GAA Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu 1820 1825 1830 | 5526 |
| GAT AGA GTC AGA GGA AGT TTT GCT TTT GAT TCA CCT CAT CAT TAC ACG Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr 1835 1840 1845 | 5574 |
| CCT ATT GAA GGA ACT CCT TAC TGT TTT TCA CGA AAT GAT TCT TTG AGT Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser 1850 1855 1860 | 5622 |

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| TCT CTA GAT TTT GAT GAT GAT GAT GTT GAC CTT TCC AGG GAA AAG GCT Ser Leu Asp Phe Asp Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala 1865 1870 1875 | 5670 |
| GAA TTA AGA AAG GCA AAA GAA AAT AAG GAA TCA GAG GCT AAA GTT ACC Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu Ser Glu Ala Lys Val Thr 1880 1885 1890 1895 | 5718 |
| AGC CAC ACA GAA CTA ACC TCC AAC CAA CAA TCA GCT AAT AAG ACA CAA Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln 1900 1905 1910 | 5766 |
| GCT ATT GCA AAG CAG CCA ATA AAT CGA GGT CAG CCT AAA CCC ATA CTT Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu 1915 1920 1925 | 5814 |
| CAG AAA CAA TCC ACT TTT CCC CAG TCA TCC AAA GAC ATA CCA GAC AGA Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser Lys Asp Ile Pro Asp Arg 1930 1935 1940 | 5862 |
| GGG GCA GCA ACT GAT GAA AAG TTA CAG AAT TTT GCT ATT GAA AAT ACT Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn Phe Ala Ile Glu Asn Thr 1945 1950 1955 | 5910 |
| CCA GTT TGC TTT TCT CAT AAT TCC TCT CTG AGT TCT CTC AGT GAC ATT Pro Val Cys Phe Ser His Asn Ser Ser Leu Ser Ser Leu Ser Asp Ile 1960 1965 1970 1975 | 5958 |
| GAC CAA GAA AAC AAC AAT AAA GAA AAT GAA CCT ATC AAA GAG ACT GAG Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu Pro Ile Lys Glu Thr Glu 1980 1985 1990 | 6006 |
| CCC CCT GAC TCA CAG GGA GAA CCA AGT AAA CCT CAA GCA TCA GGC TAT Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys Pro Gln Ala Ser Gly Tyr 1995 2000 2005 | 6054 |
| GCT CCT AAA TCA TTT CAT GTT GAA GAT ACC CCA GTT TGT TTC TCA AGA Ala Pro Lys Ser Phe His Val Glu Asp Thr Pro Val Cys Phe Ser Arg 2010 2015 2020 | 6102 |
| AAC AGT TCT CTC AGT TCT CTT AGT ATT GAC TCT GAA GAT GAC CTG TTG Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp Ser Glu Asp Asp Leu Leu 2025 2030 2035 | 6150 |
| CAG GAA TGT ATA AGC TCC GCA ATG CCA AAA AAG AAA AAG CCT TCA AGA Gln Glu Cys Ile Ser Ser Ala Met Pro Lys Lys Lys Lys Pro Ser Arg 2040 2045 2050 2055 | 6198 |

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| CTC AAG GGT GAT AAT GAA AAA CAT AGT CCC AGA AAT ATG GGT GGC ATA Leu Lys Gly Asp Asn Glu Lys His Ser Pro Arg Asn Met Gly Gly Ile 2060 2065 2070 | 6246 |
| TTA GGT GAA GAT CTG ACA CTT GAT TTG AAA GAT ATA CAG AGA CCA GAT Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys Asp Ile Gln Arg Pro Asp 2075 2080 2085 | 6294 |
| TCA GAA CAT GGT CTA TCC CCT GAT TCA GAA AAT TTT GAT TGG AAA GCT Ser Glu His Gly Leu Ser Pro Asp Ser Glu Asn Phe Asp Trp Lys Ala 2090 2095 2100 | 6342 |
| ATT CAG GAA GGT GCA AAT TCC ATA GTA AGT AGT TTA CAT CAA GCT GCT Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala 2105 2110 2115 | 6390 |
| GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile 2120 2125 2130 2135 | 6438 |
| CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr 2140 2145 2150 | 6486 |
| CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile 2155 2160 2165 | 6534 |
| CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser 2170 2175 2180 | 6582 |
| GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile 2185 2190 2195 | 6630 |
| ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln 2200 2205 2210 2215 | 6678 |
| CCC CTT CAA GCA AAC ATG CCT TCA ATC TCT CGA GGC AGG ACA ATG ATT Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile 2220 2225 2230 | 6726 |
| CAT ATT CCA GGA GTT CGA AAT AGC TCC TCA AGT ACA AGT CCT GTT TCT His Ile Pro Gly Val Arg Asn Ser Ser Ser Ser Thr Ser Pro Val Ser 2235 2240 2245 | 6774 |
| AAA AAA GGC CCA CCC CTT AAG ACT CCA GCC TCC AAA AGC CCT AGT GAA Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu 2250 2255 2260 | 6822 |

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| GGT CAA ACA GCC ACC ACT TCT CCT AGA GGA GCC AAG CCA TCT GTG AAA Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys 2265 2270 2275 | 6870 |
| TCA GAA TTA AGC CCT GTT GCC AGG CAG ACA TCC CAA ATA GGT GGG TCA Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser 2280 2285 2290 2295 | 6918 |
| AGT AAA GCA CCT TCT AGA TCA GGA TCT AGA GAT TCG ACC CCT TCA AGA Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg 2300 2305 2310 | 6966 |
| CCT GCC CAG CAA CCA TTA AGT AGA CCT ATA CAG TCT CCT GGC CGA AAC Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn 2315 2320 2325 | 7014 |
| TCA ATT TCC CCT GGT AGA AAT GGA ATA AGT CCT CCT AAC AAA TTA TCT Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser 2330 2335 2340 | 7062 |
| CAA CTT CCA AGG ACA TCA TCC CCT AGT ACT GCT TCA ACT AAG TCC TCA Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser 2345 2350 2355 | 7110 |
| GGT TCT GGA AAA ATG TCA TAT ACA TCT CCA GGT AGA CAG ATG AGC CAA Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln 2360 2365 2370 2375 | 7158 |
| CAG AAC CTT ACC AAA CAA ACA GGT TTA TCC AAG AAT GCC AGT AGT ATT Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile 2380 2385 2390 | 7206 |
| CCA AGA AGT GAG TCT GCC TCC AAA GGA CTA AAT CAG ATG AAT AAT GGT Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly 2395 2400 2405 | 7254 |
| AAT GGA GCC AAT AAA AAG GTA GAA CTT TCT AGA ATG TCT TCA ACT AAA Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys 2410 2415 2420 | 7302 |
| TCA AGT GGA AGT GAA TCT GAT AGA TCA GAA AGA CCT GTA TTA GTA CGC Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg 2425 2430 2435 | 7350 |
| CAG TCA ACT TTC ATC AAA GAA GCT CCA AGC CCA ACC TTA AGA AGA AAA Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys 2440 2445 2450 2455 | 7398 |

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| TTG GAG GAA TCT GCT TCA TTT GAA TCT CTT TCT CCA TCA TCT AGA CCA Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro 2460 2465 2470 | 7446 |
| GCT TCT CCC ACT AGG TCC CAG GCA CAA ACT CCA GTT TTA AGT CCT TCC Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser 2475 2480 2485 | 7494 |
| CTT CCT GAT ATG TCT CTA TCC ACA CAT TCG TCT GTT CAG GCT GGT GGA Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly 2490 2495 2500 | 7542 |
| TGG CGA AAA CTC CCA CCT AAT CTC AGT CCC ACT ATA GAG TAT AAT GAT Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp 2505 2510 2515 | 7590 |
| GGA AGA CCA GCA AAG CGC CAT GAT ATT GCA CGG TCT CAT TCT GAA AGT Gly Arg Pro Ala Lys Arg His Asp Ile Ala Arg Ser His Ser Glu Ser 2520 2525 2530 2535 | 7638 |
| CCT TCT AGA CTT CCA ATC AAT AGG TCA GGA ACC TGG AAA CGT GAG CAC Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly Thr Trp Lys Arg Glu His 2540 2545 2550 | 7686 |
| AGC AAA CAT TCA TCA TCC CTT CCT CGA GTA AGC ACT TGG AGA AGA ACT Ser Lys His Ser Ser Ser Leu Pro Arg Val Ser Thr Trp Arg Arg Thr 2555 2560 2565 | 7734 |
| GGA AGT TCA TCT TCA ATT CTT TCT GCT TCA TCA GAA TCC AGT GAA AAA Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser Ser Glu Ser Ser Glu Lys 2570 2575 2580 | 7782 |
| GCA AAA AGT GAG GAT GAA AAA CAT GTG AAC TCT ATT TCA GGA ACC AAA Ala Lys Ser Glu Asp Glu Lys His Val Asn Ser Ile Ser Gly Thr Lys 2585 2590 2595 | 7830 |
| CAA AGT AAA GAA AAC CAA GTA TCC GCA AAA GGA ACA TGG AGA AAA ATA Gln Ser Lys Glu Asn Gln Val Ser Ala Lys Gly Thr Trp Arg Lys Ile 2600 2605 2610 2615 | 7878 |
| AAA GAA AAT GAA TTT TCT CCC ACA AAT AGT ACT TCT CAG ACC GTT TCC Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser Thr Ser Gln Thr Val Ser 2620 2625 2630 | 7926 |
| TCA GGT GCT ACA AAT GGT GCT GAA TCA AAG ACT CTA ATT TAT CAA ATG Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys Thr Leu Ile Tyr Gln Met 2635 2640 2645 | 7974 |
| GCA CCT GCT GTT TCT AAA ACA GAG GAT GTT TGG GTG AGA ATT GAG GAC Ala Pro Ala Val Ser Lys Thr Glu Asp Val Trp Val Arg Ile Glu Asp 2650 2655 2660 | 8022 |

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| TGT CCC ATT AAC AAT CCT AGA TCT GGA AGA TCT CCC ACA GGT AAT ACT Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg Ser Pro Thr Gly Asn Thr 2665 2670 2675 | 8070 |
| CCC CCG GTG ATT GAC AGT GTT TCA GAA AAG GCA AAT CCA AAC ATT AAA Pro Pro Val Ile Asp Ser Val Ser Glu Lys Ala Asn Pro Asn Ile Lys 2680 2685 2690 2695 | 8118 |
| GAT TCA AAA GAT AAT CAG GCA AAA CAA AAT GTG GGT AAT GGC AGT GTT Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn Val Gly Asn Gly Ser Val 2700 2705 2710 | 8166 |
| CCC ATG CGT ACC GTG GGT TTG GAA AAT CGC CTG ACC TCC TTT ATT CAG Pro Met Arg Thr Val Gly Leu Glu Asn Arg Leu Thr Ser Phe Ile Gln 2715 2720 2725 | 8214 |
| GTG GAT GCC CCT GAC CAA AAA GGA ACT GAG ATA AAA CCA GGA CAA AAT Val Asp Ala Pro Asp Gln Lys Gly Thr Glu Ile Lys Pro Gly Gln Asn 2730 2735 2740 | 8262 |
| AAT CCT GTC CCT GTA TCA GAG ACT AAT GAA AGT CCT ATA GTG GAA CGT Asn Pro Val Pro Val Ser Glu Thr Asn Glu Ser Pro Ile Val Glu Arg 2745 2750 2755 | 8310 |
| ACC CCA TTC AGT TCT AGC AGC TCA AGC AAA CAC AGT TCA CCT AGT GGG Thr Pro Phe Ser Ser Ser Ser Ser Lys His Ser Ser Pro Ser Gly 2760 2765 2770 2775 | 8358 |
| ACT GTT GCT GCC AGA GTG ACT CCT TTT AAT TAC AAC CCA AGC CCT AGG Thr Val Ala Ala Arg Val Thr Pro Phe Asn Tyr Asn Pro Ser Pro Arg 2780 2785 2790 | 8406 |
| AAA AGC AGC GCA GAT AGC ACT TCA GCT CGG CCA TCT CAG ATC CCA ACT Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg Pro Ser Gln Ile Pro Thr 2795 2800 2805 | 8454 |
| CCA GTG AAT AAC AAC ACA AAG AAG CGA GAT TCC AAA ACT GAC AGC ACA Pro Val Asn Asn Asn Thr Lys Lys Arg Asp Ser Lys Thr Asp Ser Thr 2810 2815 2820 | 8502 |
| GAA TCC AGT GGA ACC CAA AGT CCT AAG CGC CAT TCT GGG TCT TAC CTT Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg His Ser Gly Ser Tyr Leu 2825 2830 2835 | 8550 |
| GTG ACA TCT GTT TAAAAGAGAG GAAGAATGAA ACTAAGAAAA TTCTATGTTA Val Thr Ser Val 2840 | 8602 |
| ATTACAACCTG CTATATAGAC ATTTTGTTC AAATGAACT TTAAAAGACT GAAAAATTTT | 8662 |
| GTAAATAGGT TTGATTCTTG TTAGAGGGTT TTTGTTCTGG AAGCCATATT TGATAGTATA | 8722 |

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| CTTTGTCTTC ACTGGTCTTA TTTTGGGAGG CACTCTTGAT GGTTAGGAAA AAATAGAAAG | 8782 |
| CCAAGTATGT TTGTACAGTA TGTTTTACAT GTATTTAAAG TAGCATCCCA TCCCAACTTC | 8842 |
| CTTAATTATT GCTTGTCTAA AATAATGAAC ACTACAGATA GGAAATATGA TATATTGCTG | 8902 |
| TTATCAATCA TTTCTAGATT ATAAACTGAC TAAACTTACA TCAGGGGAAA ATTGGTATTT | 8962 |
| ATGCAAAAAA AAAATGTTTT TGTCTTGTG AGTCCATCTA ACATCATAAT TAATCATGTG | 9022 |
| GCTGTGAAAT TCACAGTAAT ATGGTTCCCG ATGAACAAGT TTACCCAGCC TGCTTTGCTT | 9082 |
| ACTGCATGAA TGAAACTGAT GGTTC AATTT CAGAAGTAAT GATTAACAGT TATGTGGTCA | 9142 |
| CATGATGTGC ATAGAGATAG CTACAGTGTA ATAATTTACA CTATTTTGTG CTCCAAACAA | 9202 |
| AACAAAAATC TGTGTAAGT TAAAACATTG AATGAAACTA TTTTACCTGA ACTAGATTTT | 9262 |
| ATCTGAAAGT AGGTAGAATT TTTGCTATGC TGTAATTTGT TGTATATTCT GGTATTTGAG | 9322 |
| GTGAGATGGC TGCTCTTTAT TAATGAGACA TGAATTGTGT CTCAACAGAA ACTAAATGAA | 9382 |
| CATTTGAGAA TAAATTATTG CTGTATGTAA ACTGTTACTG AAATTGGTAT TTGTTTGAAG | 9442 |
| GGTTTGTTC ACATTTGTAT TAATTAATTG TTTAAAATGC CTCTTTTAAA AGCTTATATA | 9502 |
| AATTTTTTCT TCAGCTTCTA TGCATTAAGA GTAAAATTCC TCTTACTGTA ATAAAAACAT | 9562 |
| TGAAGAAGAC TGTTGCCACT TAACCATTCC ATGCGTTGGC ACTT | 9606 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Ser | Tyr | Asp | Gln | Leu | Leu | Lys | Gln | Val | Glu | Ala | Leu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Lys | Met | Glu | Asn | Ser | Asn | Leu | Arg | Gln | Glu | Leu | Glu | Asp | Asn | Ser | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Leu | Thr | Lys | Leu | Glu | Thr | Glu | Ala | Ser | Asn | Met | Lys | Glu | Val | Leu |
| | | | 35 | | | | 40 | | | | | 45 | | | |

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
 50 55 60

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
 65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
 85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
 100 105 110

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
 115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
 130 135 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
 145 150 155 160

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
 165 170 175

Asn Phe Ser Leu Gln Thr Asp Leu Thr Arg Arg Gln Leu Glu Tyr Glu
 180 185 190

Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
 195 200 205

Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile
 210 215 220

Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
 225 230 235 240

Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp
 245 250 255

Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala
 260 265 270

Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
 275 280 285

Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu
 290 295 300

Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser
 305 310 315 320

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Thr | His | Asp | Lys | Asp | Asp | Met | Ser | Arg | Thr | Leu | Leu | Ala | 325 | 330 | 335 |
| Met | Ser | Ser | Ser | Gln | Asp | Ser | Cys | Ile | Ser | Met | Arg | Gln | Ser | Gly | Cys | 340 | 345 | 350 |
| Leu | Pro | Leu | Leu | Ile | Gln | Leu | Leu | His | Gly | Asn | Asp | Lys | Asp | Ser | Val | 355 | 360 | 365 |
| Leu | Leu | Gly | Asn | Ser | Arg | Gly | Ser | Lys | Glu | Ala | Arg | Ala | Arg | Ala | Ser | 370 | 375 | 380 |
| Ala | Ala | Leu | His | Asn | Ile | Ile | His | Ser | Gln | Pro | Asp | Asp | Lys | Arg | Gly | 385 | 390 | 395 |
| Arg | Arg | Glu | Ile | Arg | Val | Leu | His | Leu | Leu | Glu | Gln | Ile | Arg | Ala | Tyr | 405 | 410 | 415 |
| Cys | Glu | Thr | Cys | Trp | Glu | Trp | Gln | Glu | Ala | His | Glu | Pro | Gly | Met | Asp | 420 | 425 | 430 |
| Gln | Asp | Lys | Asn | Pro | Met | Pro | Ala | Pro | Val | Glu | His | Gln | Ile | Cys | Pro | 435 | 440 | 445 |
| Ala | Val | Cys | Val | Leu | Met | Lys | Leu | Ser | Phe | Asp | Glu | Glu | His | Arg | His | 450 | 455 | 460 |
| Ala | Met | Asn | Glu | Leu | Gly | Gly | Leu | Gln | Ala | Ile | Ala | Glu | Leu | Leu | Gln | 465 | 470 | 475 |
| Val | Asp | Cys | Glu | Met | Tyr | Gly | Leu | Thr | Asn | Asp | His | Tyr | Ser | Ile | Thr | 485 | 490 | 495 |
| Leu | Arg | Arg | Tyr | Ala | Gly | Met | Ala | Leu | Thr | Asn | Leu | Thr | Phe | Gly | Asp | 500 | 505 | 510 |
| Val | Ala | Asn | Lys | Ala | Thr | Leu | Cys | Ser | Met | Lys | Gly | Cys | Met | Arg | Ala | 515 | 520 | 525 |
| Leu | Val | Ala | Gln | Leu | Lys | Ser | Glu | Ser | Glu | Asp | Leu | Gln | Gln | Val | Ile | 530 | 535 | 540 |
| Ala | Ser | Val | Leu | Arg | Asn | Leu | Ser | Trp | Arg | Ala | Asp | Val | Asn | Ser | Lys | 545 | 550 | 555 |
| Lys | Thr | Leu | Arg | Glu | Val | Gly | Ser | Val | Lys | Ala | Leu | Met | Glu | Cys | Ala | 565 | 570 | 575 |
| Leu | Glu | Val | Lys | Lys | Glu | Ser | Thr | Leu | Lys | Ser | Val | Leu | Ser | Ala | Leu | 580 | 585 | 590 |

Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala
 595 600 605
 Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser
 610 615 620
 Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg
 625 630 635 640
 Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu
 645 650 655
 Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His
 660 665 670
 Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser
 675 680 685
 Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val
 690 695 700
 Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met
 705 710 715 720
 Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
 725 730 735
 Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
 740 745 750
 His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His
 755 760 765
 Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser
 770 775 780
 His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val
 785 790 795 800
 Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr
 805 810 815
 Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro
 820 825 830
 Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
 835 840 845
 Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
 850 855 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
 865 870 875 880
 Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
 885 890 895
 Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
 900 905 910
 His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
 915 920 925
 His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
 930 935 940
 Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
 945 950 955 960
 Asn Asp Ser Leu Asn Ser Val Ser Ser Asn Asp Gly Tyr Gly Lys Arg
 965 970 975
 Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
 980 985 990
 Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
 995 1000 1005
 His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
 1010 1015 1020
 Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
 1025 1030 1035 1040
 Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
 1045 1050 1055
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
 1060 1065 1070
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
 1075 1080 1085
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
 1090 1095 1100
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly
 1105 1110 1115 1120
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
 1125 1130 1135

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|
| Asp | Asp | Lys | Pro | Thr | Asn | Tyr | Ser | Glu | Arg | Tyr | Ser | Glu | Glu | Glu | Gln | 1140 | 1145 | 1150 |
| His | Glu | Glu | Glu | Glu | Arg | Pro | Thr | Asn | Tyr | Ser | Ile | Lys | Tyr | Asn | Glu | 1155 | 1160 | 1165 |
| Glu | Lys | Arg | His | Val | Asp | Gln | Pro | Ile | Asp | Tyr | Ser | Leu | Lys | Tyr | Ala | 1170 | 1175 | 1180 |
| Thr | Asp | Ile | Pro | Ser | Ser | Gln | Lys | Gln | Ser | Phe | Ser | Phe | Ser | Lys | Ser | 1185 | 1190 | 1195 |
| Ser | Ser | Gly | Gln | Ser | Ser | Lys | Thr | Glu | His | Met | Ser | Ser | Ser | Ser | Glu | 1205 | 1210 | 1215 |
| Asn | Thr | Ser | Thr | Pro | Ser | Ser | Asn | Ala | Lys | Arg | Gln | Asn | Gln | Leu | His | 1220 | 1225 | 1230 |
| Pro | Ser | Ser | Ala | Gln | Ser | Arg | Ser | Gly | Gln | Pro | Gln | Lys | Ala | Ala | Thr | 1235 | 1240 | 1245 |
| Cys | Lys | Val | Ser | Ser | Ile | Asn | Gln | Glu | Thr | Ile | Gln | Thr | Tyr | Cys | Val | 1250 | 1255 | 1260 |
| Glu | Asp | Thr | Pro | Ile | Cys | Phe | Ser | Arg | Cys | Ser | Ser | Leu | Ser | Ser | Leu | 1265 | 1270 | 1275 |
| Ser | Ser | Ala | Glu | Asp | Glu | Ile | Gly | Cys | Asn | Gln | Thr | Thr | Gln | Glu | Ala | 1285 | 1290 | 1295 |
| Asp | Ser | Ala | Asn | Thr | Leu | Gln | Ile | Ala | Glu | Ile | Lys | Gly | Lys | Ile | Gly | 1300 | 1305 | 1310 |
| Thr | Arg | Ser | Ala | Glu | Asp | Pro | Val | Ser | Glu | Val | Pro | Ala | Val | Ser | Gln | 1315 | 1320 | 1325 |
| His | Pro | Arg | Thr | Lys | Ser | Ser | Arg | Leu | Gln | Gly | Ser | Ser | Leu | Ser | Ser | 1330 | 1335 | 1340 |
| Glu | Ser | Ala | Arg | His | Lys | Ala | Val | Glu | Phe | Pro | Ser | Gly | Ala | Lys | Ser | 1345 | 1350 | 1355 |
| Pro | Ser | Lys | Ser | Gly | Ala | Gln | Thr | Pro | Lys | Ser | Pro | Pro | Glu | His | Tyr | 1365 | 1370 | 1375 |
| Val | Gln | Glu | Thr | Pro | Leu | Met | Phe | Ser | Arg | Cys | Thr | Ser | Val | Ser | Ser | 1380 | 1385 | 1390 |
| Leu | Asp | Ser | Phe | Glu | Ser | Arg | Ser | Ile | Ala | Ser | Ser | Val | Gln | Ser | Glu | 1395 | 1400 | 1405 |

Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
 1410 1415 1420

Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
 1425 1430 1435 1440

Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys
 1445 1450 1455

Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val
 1460 1465 1470

Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu
 1475 1480 1485

Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser
 1490 1495 1500

Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val
 1505 1510 1515 1520

Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu
 1525 1530 1535

Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu
 1540 1545 1550

Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp
 1555 1560 1565

Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro
 1570 1575 1580

Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys
 1585 1590 1595 1600

Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys
 1605 1610 1615

Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe
 1620 1625 1630

Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro
 1635 1640 1645

Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser
 1650 1655 1660

Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln
 1665 1670 1675 1680

Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser
 1685 1690 1695

Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu
 1700 1705 1710

Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile
 1715 1720 1725

Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys
 1730 1735 1740

Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro
 1745 1750 1755 1760

Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val
 1765 1770 1775

Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn
 1780 1785 1790

Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn
 1795 1800 1805

Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn
 1810 1815 1820

Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe
 1825 1830 1835 1840

Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe
 1845 1850 1855

Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val
 1860 1865 1870

Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys
 1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln
 1890 1895 1900

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg
 1905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser
 1925 1930 1935

Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln
 1940 1945 1950

| | | |
|---|-----------|-----------|
| Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser | | |
| 1955 | 1960 | 1965 |
| Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn | | |
| 1970 | 1975 | 1980 |
| Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser | | |
| 1985 | 1990 | 1995 2000 |
| Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp | | |
| | 2005 2010 | 2015 |
| Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile | | |
| | 2020 2025 | 2030 |
| Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro | | |
| | 2035 2040 | 2045 |
| Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser | | |
| | 2050 2055 | 2060 |
| Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu | | |
| | 2065 2070 | 2075 2080 |
| Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser | | |
| | 2085 2090 | 2095 |
| Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val | | |
| | 2100 2105 | 2110 |
| Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala | | |
| | 2115 2120 | 2125 |
| Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu | | |
| | 2130 2135 | 2140 |
| Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr | | |
| | 2145 2150 | 2155 2160 |
| Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu | | |
| | 2165 2170 | 2175 |
| Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys | | |
| | 2180 2185 | 2190 |
| Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu | | |
| | 2195 2200 | 2205 |
| Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile | | |
| | 2210 2215 | 2220 |

Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
 2225 2230 2235 2240
 Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
 2245 2250 2255
 Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
 2260 2265 2270
 Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln
 2275 2280 2285
 Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
 2290 2295 2300
 Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro
 2305 2310 2315 2320
 Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
 2325 2330 2335
 Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
 2340 2345 2350
 Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
 2355 2360 2365
 Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
 2370 2375 2380
 Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
 2385 2390 2395 2400
 Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
 2405 2410 2415
 Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
 2420 2425 2430
 Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
 2435 2440 2445
 Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
 2450 2455 2460
 Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
 2465 2470 2475 2480
 Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
 2485 2490 2495

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
 2500 2505 2510

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
 2515 2520 2525

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
 2530 2535 2540

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
 2545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
 2565 2570 2575

Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
 2580 2585 2590

Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
 2595 2600 2605

Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
 2610 2615 2620

Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
 2625 2630 2635 2640

Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
 2645 2650 2655

Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
 2660 2665 2670

Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
 2675 2680 2685

Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
 2690 2695 2700

Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
 2705 2710 2715 2720

Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
 2725 2730 2735

Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn
 2740 2745 2750

Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser
 2755 2760 2765

Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe
 2770 2775 2780
 Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala
 2785 2790 2795 2800
 Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg
 2805 2810 2815
 Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys
 2820 2825 2830
 Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
 2835 2840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DP1(TB2)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC | 48 |
| Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly | |
| 1 5 10 15 | |
| GAG ACG GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG | 96 |
| Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg | |
| 20 25 30 | |
| TTC CTG CAC GAG AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG | 144 |
| Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu | |
| 35 40 45 | |

| | |
|---|-----|
| GCC AAA ACC GGC GTG AAC AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly 50 55 60 | 192 |
| CTG GTG GCC TTG TAC CTG GTG TTC GGT TAT GGA GCC TCT CTC CTC TGC Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys 65 70 75 80 | 240 |
| AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC ATC TCA ATT AAA GCT ATA Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile 85 90 95 | 288 |
| GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG ACC TAC TGG GTA Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu Thr Tyr Trp Val 100 105 110 | 336 |
| GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC TTC CTG Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu 115 120 125 | 384 |
| TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp 130 135 140 | 432 |
| TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg 145 150 155 160 | 480 |
| ATC ATC CGT CCT TTC TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val 165 170 175 | 528 |
| GTC AAG GAC CTT AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr 180 185 190 | 576 |
| AAA GAA GCG AAG AAA GCT ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys 195 200 205 | 624 |
| AGC ACC TAAACCAGAC TAAACCAGAC TGGATGGAAA CTCCTGCCC TCTCTGTACC Ser Thr 210 | 680 |
| TTCTACTGG AGCTTGATGT TATATTAGGG ACTGTGGTAT AATTATTTTA ATAATGTTGC | 740 |
| CTTGGAACA TTTTGTAGAT ATTAAAGATT GGAATGTGTT GTAAGTTTCT TTGCTTACTT | 800 |
| TTACTGTCTA TATATATAGG GAGCACTTTA AACTTAATGC AGTGGGCAGT GTCCACGTTT | 860 |
| TTGGAAAATG TATTTTGCCT CTGGGTAGGA AAAGATGTAT GTTGCTATCC TGCAGGAAAT | 920 |

| | |
|--|------|
| ATAAACTTAA AATAAAATTA TATACCCAC AGGCTGTGTA CTTTACTGGG CTCTCCCTGC | 980 |
| ACGSATTTTC TCTGTAGTTA CATTTAGGRT AATCTTTATG GTTCTACTTC CTRTAATGTA | 1040 |
| CAATTTTATA TAATTCNGRA ATGTTTTTAA TGTATTTGTG CACATGTACA TATGGAAATG | 1100 |
| TTACTGTCTG ACTACANCAT GCATCATGCT CATGGGGAGG GAGCAGGGGA AGGTTGTATG | 1160 |
| TGTCATTTAT AACTTCTGTA CAGTAAGACC ACCTGCCAAA AGCTGGAGGA ACCATTGTGC | 1220 |
| TGGTGTGGTC TACTAAATAA TACTTTAGGA AATACGTGAT TAATATGCAA GTGAACAAAG | 1280 |
| TGAGAAATGA AATCGAATGG AGATTGGCCT GGTGTGTTCC GTAGTATATG GCATATGAAT | 1340 |
| ACCAGGATAG CTTTATAAAG CAGTTAGTTA GTTAGTTACT CACTCTAGTG ATAAATCGGG | 1400 |
| AAATTTACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAG | 1460 |
| AGTACCCTGT AACTCTCAAT TCCCTGAAAA ACTAGTAATA CTGTCTTATC TGCTATAAAC | 1520 |
| TTTACATATT TGTCTATTGT CAAGATGCTA CANTGGAMNC CATTTCTGGT TTTATCTTCA | 1580 |
| NAGSGGAGAN ACATGTTGAT TTAGTCTTCT TTCCCAATCT TCTTTTTTAA MCCAGTTTNA | 1640 |
| GGMNCTTCTG RAGATTTGYC CACCTCTGAT TACATGTATG TTCTYGTTTG TATCATKAGC | 1700 |
| AACAACATGC TAATGRCGAC ACCTAGCTCT RAGMCAATT CTGGGAGANT GARAGGNWGT | 1760 |
| ATARAGTMNC CCATAATCTG CTTGGCAATA GTTAAGTCAA TCTATCTTCA GTTTTTCTCT | 1820 |
| GGCCTTTAAG GTCAAACACA AGAGGCTTCC CTAGTTTACA AGTCAGAGTC ACTTGTAAGTC | 1880 |
| CATTTAAATG CCCTCATCCG TATTC'TTTGT GTTGATAAGC TGCACAKGAC TACATAGTAA | 1940 |
| GTACAGANCA GTAAAGTTAA NNCGGATGTC TCCATTGATC TGCCAANTCG NTATAGAGAG | 2000 |
| CAATTTGTCT GGACTIONAAA ATCTGAGTTT TACACCATAC TGTTAAGAGT CCTTTTGAAT | 2060 |
| TAAACTAGAC TAAAACAAGT GTATAACTAA ACTAACAAGA TTAAATATCC AGCCAGTACA | 2120 |
| GTATTTTTTA AGGCAAATAA AGATGATTAG CTCACCTTGA GNTAACAATC AGGTAAGATC | 2180 |
| ATNACAATGT CTCATGATGT NAANAATATT AAAGATATCA ATACTAAGTG ACAGTATCAC | 2240 |
| NNCTAATATA ATATGGATCA GAGCATTTAT TTTGGGGAGG AAAACAGTGG TGATTACCGG | 2300 |
| CATTTTATTA AACTTAAAC TTTGTAGAAA GCAAACAAAA TTGTTCTTGG GAGAAAATCA | 2360 |
| ACTTTTAGAT TAAAAAATT TTAAGTAWCT AGGAGTATTT AAATCCTTTT CCCATAAATA | 2420 |

AAAGTACAGT TTTCTTGGTG GCAGAATGAA AATCAGCAAC NTCTAGCATA TAGACTATAT 2480
 AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC 2540
 TATTGCTCAT AATGACTTAC AGGCTAAAAAN TAGNTNTAAA ATACTATATT AAATTCTGAA 2600
 TGCAATTTTT TTTTGTTCCT TTGAGACCAA AATTTAAGTT AACTGTTGCT GGCAGTCTAA 2660
 GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTTCCTCA 2720
 AATGAAATAC TGCCTTGGCT AGAGTTTGAA AAATAATTG AGCCTGTGCC TGGCTAGAAA 2780
 ACAAGCGTTT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATTCCTACC 2840
 AAACAGCTTA AATTCTTCAA GAAAGAATTC CTGCAGCAGT TATTCCCTTA CCTGAAGGCT 2900
 TCAATCATTT GGATCAACAA CTGCTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA 2960
 AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA 3020
 AATAAATAGA TGTAATAAAA ATTGAGWTCT CATTTAAAAA AAACCATGTG CCCAATGGGA 3080
 AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT 3140
 ANCCTATATA TACATCTCTG TCAGTGCCCC TC 3172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly
 1 5 10 15
 Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg
 20 25 30
 Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu
 35 40 45
 Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly
 50 55 60
 Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | 70 | | 75 | | 80 | | | | | | | | | |
| Asn | Leu | Ile | Gly | Phe | Gly | Tyr | Pro | Ala | Tyr | Ile | Ser | Ile | Lys | Ala | Ile |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Glu | Ser | Pro | Asn | Lys | Glu | Asp | Asp | Thr | Gln | Trp | Leu | Thr | Tyr | Trp | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Tyr | Gly | Val | Phe | Ser | Ile | Ala | Glu | Phe | Phe | Ser | Asp | Ile | Phe | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Trp | Phe | Pro | Phe | Tyr | Tyr | Met | Leu | Lys | Cys | Gly | Phe | Leu | Leu | Trp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Cys | Met | Ala | Pro | Ser | Pro | Ser | Asn | Gly | Ala | Glu | Leu | Leu | Tyr | Lys | Arg |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Ile | Arg | Pro | Phe | Phe | Leu | Lys | His | Glu | Ser | Gln | Met | Asp | Ser | Val |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Val | Lys | Asp | Leu | Lys | Asp | Lys | Ser | Lys | Glu | Thr | Ala | Asp | Ala | Ile | Thr |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Lys | Glu | Ala | Lys | Lys | Ala | Thr | Val | Asn | Leu | Leu | Gly | Glu | Glu | Lys | Lys |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Ser | Thr | | | | | | | | | | | | | | |
| | 210 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Pro | Val | Val | Val | Gly | Ser | Gly | Arg | Ala | Pro | Arg | His | Pro | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Pro Ala Ala Met His Pro Arg Arg Pro Asp Gly Phe Asp Gly Leu Gly
 20 25 30
 Tyr Arg Gly Gly Ala Arg Asp Glu Gln Gly Phe Gly Gly Ala Phe Pro
 35 40 45
 Ala Arg Ser Phe Ser Thr Gly Ser Asp Leu Gly His Trp Val Thr Thr
 50 55 60
 Pro Pro Asp Ile Pro Gly Ser Arg Asn Leu His Trp Gly Glu Lys Ser
 65 70 75 80
 Pro Pro Tyr Gly Val Pro Thr Thr Ser Thr Pro Tyr Glu Gly Pro Thr
 85 90 95
 Glu Glu Pro Phe Ser Ser Gly Gly Gly Gly Ser Val Gln Gly Gln Ser
 100 105 110
 Ser Glu Gln Leu Asn Arg Phe Ala Gly Phe Gly Ile Gly Leu Ala Ser
 115 120 125
 Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu Arg Arg
 130 135 140
 Gln Cys Gln Val Asn Tyr His Ala Gln His Tyr His Leu Thr Pro Phe
 145 150 155 160
 Thr Val Ile Asn Ile Met Tyr Ser Phe Asn Lys Thr Gln Gly Pro Arg
 165 170 175
 Ala Leu Trp Lys Gly Met Gly Ser Thr Phe Ile Val Gln Gly Val Thr
 180 185 190
 Leu Gly Ala Glu Gly Ile Ile Ser Glu Phe Thr Pro Leu Pro Arg Glu
 195 200 205
 Val Leu His Lys Trp Ser Pro Lys Gln Ile Gly Glu His Leu Leu Leu
 210 215 220
 Lys Ser Leu Thr Tyr Val Val Ala Met Pro Phe Tyr Ser Ala Ser Leu
 225 230 235 240
 Ile Glu Thr Val Gln Ser Glu Ile Ile Arg Asp Asn Thr Gly Ile Leu
 245 250 255
 Glu Cys Val Lys Glu Gly Ile Gly Arg Val Ile Gly Met Gly Val Pro
 260 265 270
 His Ser Lys Arg Leu Leu Pro Leu Leu Ser Leu Ile Phe Pro Thr Val
 275 280 285

Leu His Gly Val Leu His Tyr Ile Ile Ser Ser Val Ile Gln Lys Phe
 290 295 300
 Val Leu Leu Ile Leu Lys Arg Lys Thr Tyr Asn Ser His Leu Ala Glu
 305 310 315 320
 Ser Thr Ser Pro Val Gln Ser Met Leu Asp Ala Tyr Phe Pro Glu Leu
 325 330 335
 Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr Pro
 340 345 350
 Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile
 355 360 365
 Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln
 370 375 380
 Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly
 385 390 395 400
 Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr
 405 410 415
 Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu
 420 425 430
 Leu Gln

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: YS-39(TB2)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Arg | Arg | Phe | Asp | Arg | Phe | Leu | His | Glu | Lys | Asn | Cys | Met | Thr | 1 | 5 | 10 | 15 |
| Asp | Leu | Leu | Ala | Lys | Leu | Glu | Ala | Lys | Thr | Gly | Val | Asn | Arg | Ser | Phe | 20 | 25 | 30 | |
| Ile | Ala | Leu | Gly | Val | Ile | Gly | Leu | Val | Ala | Leu | Tyr | Leu | Val | Phe | Gly | 35 | 40 | 45 | |
| Tyr | Gly | Ala | Ser | Leu | Leu | Cys | Asn | Leu | Ile | Gly | Phe | Gly | Tyr | Pro | Ala | 50 | 55 | 60 | |
| Tyr | Ile | Ser | Ile | Lys | Ala | Ile | Glu | Ser | Pro | Asn | Lys | Glu | Asp | Asp | Thr | 65 | 70 | 75 | 80 |
| Gln | Trp | Leu | Thr | Tyr | Trp | Val | Val | Tyr | Gly | Val | Phe | Ser | Ile | Ala | Glu | 85 | 90 | 95 | |
| Phe | Phe | Ser | Asp | Ile | Phe | Leu | Ser | Trp | Phe | Pro | Phe | Tyr | Tyr | Ile | Leu | 100 | 105 | 110 | |
| Lys | Cys | Gly | Phe | Leu | Leu | Trp | Cys | Met | Ala | Pro | Ser | Pro | Ser | Asn | Gly | 115 | 120 | 125 | |
| Ala | Glu | Leu | Leu | Tyr | Lys | Arg | Ile | Ile | Arg | Pro | Phe | Phe | Leu | Lys | His | 130 | 135 | 140 | |
| Glu | Ser | Gln | Met | Asp | Ser | Val | Val | Lys | Asp | Leu | Lys | Asp | Lys | Ala | Lys | 145 | 150 | 155 | 160 |
| Glu | Thr | Ala | Asp | Ala | Ile | Thr | Lys | Glu | Ala | Lys | Lys | Ala | Thr | Val | Asn | 165 | 170 | 175 | |
| Leu | Leu | Gly | Glu | Glu | Lys | Lys | Ser | Thr | 180 | 185 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: [2842] 2843 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: APC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|
| Met | Ala | Ala | Ala | Ser | Tyr | Asp | Gln | Leu | Leu | Lys | Gln | Val | Glu | Ala | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Met | Glu | Asn | Ser | Asn | Leu | Arg | Gln | Glu | Leu | Glu | Asp | Asn | Ser | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Leu | Thr | Lys | Leu | Glu | Thr | Glu | Ala | Ser | Asn | Met | Lys | Glu | Val | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Gln | Leu | Gln | Gly | Ser | Ile | Glu | Asp | Glu | Ala | Met | Ala | Ser | Ser | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Ile | Asp | Leu | Leu | Glu | Arg | Leu | Lys | Glu | Leu | Asn | Leu | Asp | Ser | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asn | Phe | Pro | Gly | Val | Lys | Leu | Arg | Ser | Lys | Met | Ser | Leu | Arg | Ser | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Ser | Arg | Glu | Gly | Ser | Val | Ser | Ser | Arg | Ser | Gly | Glu | Cys | Ser | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Pro | Met | Gly | Ser | Phe | Pro | Arg | Arg | Gly | Phe | Val | Asn | Gly | Ser | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Glu | Ser | Thr | Gly | Tyr | Leu | Glu | Glu | Leu | Glu | Lys | Glu | Arg | Ser | Leu | Leu |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Leu | Ala | Asp | Leu | Asp | Lys | Glu | Glu | Lys | Glu | Lys | Asp | Trp | Tyr | Tyr | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gln | Leu | Gln | Asn | Leu | Thr | Lys | Arg | Ile | Asp | Ser | Leu | [Leu | Thr | Glu | Asn |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Ser | Leu | Gln | Thr | Asp | Met | Thr | Arg | Arg | Gln | Leu | Glu | Tyr | Glu | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Gln | Ile | Arg | Val | Ala | Met | Glu | Glu | Gln | Leu | Gly | Thr | Cys | Gln | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Met | Glu | Lys | Arg | Ala | Gln | Arg | Arg | Ile | Ala | Arg | Ile | Gln | Gln | Ile | Glu |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| Lys | Asp | Ile | Leu | Arg | Ile | Arg | Gln | Leu | Leu | Gln | Ser | Gln | Ala | Thr | Glu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ala | Glu | Arg | Ser | Ser | Gln | Asn | Lys | His | Glu | Thr | Gly | Ser | His | Asp | Ala |

| 245 | | | | | | | | | | 250 | | | | | 255 | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Glu | Arg | Gln | Asn | Glu | Gly | Gln | Gly | Val | Gly | Glu | Ile | Asn | Met | Ala | Thr | | | | | | | | | | | | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | | | | | | | | | | | | |
| Ser | Gly | Asn | Gly | Gln | Gly | Ser | Thr | Thr | Arg | Met | Asp | His | Glu | Thr | Ala | | | | | | | | | | | | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | | | | | | | | | | | | |
| Ser | Val | Leu | Ser | Ser | Ser | Ser | Thr | His | Ser | Ala | Pro | Arg | Arg | Leu | Thr | | | | | | | | | | | | | | | |
| | 290 | | | | | | 295 | | | | 300 | | | | | | | | | | | | | | | | | | | |
| Ser | His | Leu | Gly | Thr | Lys | Val | Glu | Met | Val | Tyr | Ser | Leu | Leu | Ser | Met | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | 315 | | | | | 320 | | | | | | | | | | | | | | | | |
| Leu | Gly | Thr | His | Asp | Lys | Asp | Asp | Met | Ser | Arg | Thr | Leu | Leu | Ala | Met | | | | | | | | | | | | | | | |
| | | | 325 | | | | | 330 | | | | | | 335 | | | | | | | | | | | | | | | | |
| Ser | Ser | Ser | Gln | Asp | Ser | Cys | Ile | Ser | Met | Arg | Gln | Ser | Gly | Cys | Leu | | | | | | | | | | | | | | | |
| | | 340 | | | | | 345 | | | | | | 350 | | | | | | | | | | | | | | | | | |
| Pro | Leu | Leu | Ile | Gln | Leu | Leu | His | Gly | Asn | Asp | Lys | Asp | Ser | Val | Leu | | | | | | | | | | | | | | | |
| | 355 | | | | | | 360 | | | | | 365 | | | | | | | | | | | | | | | | | | |
| Leu | Gly | Asn | Ser | Arg | Gly | Ser | Lys | Glu | Ala | Arg | Ala | Arg | Ala | Ser | Ala | | | | | | | | | | | | | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | | | | | | | | | | | | | | |
| Ala | Leu | His | Asn | Ile | Ile | His | Ser | Gln | Pro | Asp | Asp | Lys | Arg | Gly | Arg | | | | | | | | | | | | | | | |
| 385 | | | | 390 | | | | | 395 | | | | | 400 | | | | | | | | | | | | | | | | |
| Arg | Glu | Ile | Arg | Val | Leu | His | Leu | Leu | Glu | Gln | Ile | Arg | Ala | Tyr | Cys | | | | | | | | | | | | | | | |
| | | | 405 | | | | | 410 | | | | | | 415 | | | | | | | | | | | | | | | | |
| Glu | Thr | Cys | Trp | Glu | Trp | Gln | Glu | Ala | His | Glu | Pro | Gly | Met | Asp | Gln | | | | | | | | | | | | | | | |
| | | 420 | | | | | 425 | | | | | | 430 | | | | | | | | | | | | | | | | | |
| Asp | Lys | Asn | Pro | Met | Pro | Ala | Pro | Val | Glu | His | Gln | Ile | Cys | Pro | Ala | | | | | | | | | | | | | | | |
| | 435 | | | | | | 440 | | | | | 445 | | | | | | | | | | | | | | | | | | |
| Val | Cys | Val | Leu | Met | Lys | Leu | Ser | Phe | Asp | Glu | Glu | His | Arg | His | Ala | | | | | | | | | | | | | | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | | | | | | | | | | | | | | |
| Met | Asn | Glu | Leu | Gly | Gly | Leu | Gln | Ala | Ile | Ala | Glu | Leu | Leu | Gln | Val | | | | | | | | | | | | | | | |
| 465 | | | | 470 | | | | | 475 | | | | | 480 | | | | | | | | | | | | | | | | |
| Asp | Cys | Glu | Met | Tyr | Gly | Leu | Thr | Asn | Asp | His | Tyr | Ser | Ile | Thr | Leu | | | | | | | | | | | | | | | |
| | | | 485 | | | | | 490 | | | | | 495 | | | | | | | | | | | | | | | | | |
| Arg | Arg | Tyr | Ala | Gly | Met | Ala | Leu | Thr | Asn | Leu | Thr | Phe | Gly | Asp | Val | | | | | | | | | | | | | | | |
| | | 500 | | | | | | 505 | | | | | 510 | | | | | | | | | | | | | | | | | |
| Ala | Asn | Lys | Ala | Thr | Leu | Cys | Ser | Met | Lys | Gly | Cys | Met | Arg | Ala | Leu | | | | | | | | | | | | | | | |

| 515 | | | | | 520 | | | | | 525 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Gln | Leu | Lys | Ser | Glu | Ser | Glu | Asp | Leu | Gln | Gln | Val | Ile | Ala |
| 530 | | | | | | 535 | | | | | 540 | | | | |
| Ser | Val | Leu | Arg | Asn | Leu | Ser | Trp | Arg | Ala | Asp | Val | Asn | Ser | Lys | Lys |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Thr | Leu | Arg | Glu | Val | Gly | Ser | Val | Lys | Ala | Leu | Met | Glu | Cys | Ala | Leu |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Glu | Val | Lys | Lys | Glu | Ser | Thr | Leu | Lys | Ser | Val | Leu | Ser | Ala | Leu | Trp |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Asn | Leu | Ser | Ala | His | Cys | Thr | Glu | Asn | Lys | Ala | Asp | Ile | Cys | Ala | Val |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Asp | Gly | Ala | Leu | Ala | Phe | Leu | Val | Gly | Thr | Leu | Thr | Tyr | Arg | Ser | Gln |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Thr | Asn | Thr | Leu | Ala | Ile | Ile | Glu | Ser | Gly | Gly | Gly | Ile | Leu | Arg | Asn |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Val | Ser | Ser | Leu | Ile | Ala | Thr | Asn | Glu | Asp | His | Arg | Gln | Ile | Leu | Arg |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Glu | Asn | Asn | Cys | Leu | Gln | Thr | Leu | Leu | Gln | His | Leu | Lys | Ser | His | Ser |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Leu | Thr | Ile | Val | Ser | Asn | Ala | Cys | Gly | Thr | Leu | Trp | Asn | Leu | Ser | Ala |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Arg | Asn | Pro | Lys | Asp | Gln | Glu | Ala | Leu | Trp | Asp | Met | Gly | Ala | Val | Ser |
| | | 690 | | | | 695 | | | | | 700 | | | | |
| Met | Leu | Lys | Asn | Leu | Ile | His | Ser | Lys | His | Lys | Met | Ile | Ala | Met | Gly |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| Ser | Ala | Ala | Ala | Leu | Arg | Asn | Leu | Met | Ala | Asn | Arg | Pro | Ala | Lys | Tyr |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Lys | Asp | Ala | Asn | Ile | Met | Ser | Pro | Gly | Ser | Ser | Leu | Pro | Ser | Leu | His |
| | | | 740 | | | | | 745 | | | | | 750 | | |
| Val | Arg | Lys | Gln | Lys | Ala | Leu | Glu | Ala | Glu | Leu | Asp | Ala | Gln | His | Leu |
| | | 755 | | | | | 760 | | | | | 765 | | | |
| Ser | Glu | Thr | Phe | Asp | Asn | Ile | Asp | Asn | Leu | Ser | Pro | Lys | Ala | Ser | His |
| | 770 | | | | | 775 | | | | | 780 | | | | |
| Arg | Ser | Lys | Gln | Arg | His | Lys | Gln | Ser | Leu | Tyr | Gly | Asp | Tyr | Val | Phe |

| | | | | | | |
|---|------|------|--|------|--|------|
| 785 | | 790 | | 795 | | 800 |
| Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly | | | | | | |
| | 805 | | | 810 | | 815 |
| Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser | | | | | | |
| | 820 | | | 825 | | 830 |
| Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp | | | | | | |
| | 835 | | | 840 | | 845 |
| Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro | | | | | | |
| | 850 | | | 855 | | 860 |
| Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser | | | | | | |
| | 865 | | | 870 | | 875 |
| Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile | | | | | | |
| | | 885 | | 890 | | 895 |
| His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His | | | | | | |
| | 900 | | | 905 | | 910 |
| Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His | | | | | | |
| | 915 | | | 920 | | 925 |
| Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg | | | | | | |
| | 930 | | | 935 | | 940 |
| Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn | | | | | | |
| | 945 | | | 950 | | 955 |
| Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly | | | | | | |
| | | 965 | | 970 | | 975 |
| Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys | | | | | | |
| | | 980 | | 985 | | 990 |
| Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His | | | | | | |
| | 995 | | | 1000 | | 1005 |
| Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile | | | | | | |
| | 1010 | | | 1015 | | 1020 |
| Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln | | | | | | |
| | 1025 | | | 1030 | | 1035 |
| Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu | | | | | | |
| | | 1045 | | 1050 | | 1055 |
| Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr | | | | | | |

| 1060 | | | | | 1065 | | | | | 1070 | | | | | | |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|
| Thr | Tyr | Pro | Val | Tyr | Thr | Glu | Ser | Thr | Asp | Asp | Lys | His | Leu | Lys | Phe | |
| 1075 | | | | | 1080 | | | | | 1085 | | | | | | |
| Gln | Pro | His | Phe | Gly | Gln | Gln | Glu | Cys | Val | Ser | Pro | Tyr | Arg | Ser | Arg | |
| 1090 | | | | | 1095 | | | | | 1100 | | | | | | |
| Gly | Ala | Asn | Gly | Ser | Glu | Thr | Asn | Arg | Val | Gly | Ser | Asn | His | Gly | Ile | |
| 1105 | | | | | 1110 | | | | | 1115 | | | | | 1120 | |
| Asn | Gln | Asn | Val | Ser | Gln | Ser | Leu | Cys | Gln | Glu | Asp | Asp | Tyr | Glu | Asp | |
| 1125 | | | | | 1130 | | | | | 1135 | | | | | | |
| Asp | Lys | Pro | Thr | Asn | Tyr | Ser | Glu | Arg | Tyr | Ser | Glu | Glu | Glu | Gln | His | |
| 1140 | | | | | 1145 | | | | | 1150 | | | | | | |
| Glu | Glu | Glu | Glu | Arg | Pro | Thr | Asn | Tyr | Ser | Ile | Lys | Tyr | Asn | Glu | Glu | |
| 1155 | | | | | 1160 | | | | | 1165 | | | | | | |
| Lys | Arg | His | Val | Asp | Gln | Pro | Ile | Asp | Tyr | Ser | Leu | Lys | Tyr | Ala | Thr | |
| 1170 | | | | | 1175 | | | | | 1180 | | | | | | |
| Asp | Ile | Pro | Ser | Ser | Gln | Lys | Gln | Ser | Phe | Ser | Phe | Ser | Lys | Ser | Ser | |
| 1185 | | | | | 1190 | | | | | 1195 | | | | | 1200 | |
| Ser | Gly | Gln | Ser | Ser | Lys | Thr | Glu | His | Met | Ser | Ser | Ser | Ser | Glu | Asn | |
| 1205 | | | | | 1210 | | | | | 1215 | | | | | | |
| Thr | Ser | Thr | Pro | Ser | Ser | Asn | Ala | Lys | Arg | Gln | Asn | Gln | Leu | His | Pro | |
| 1220 | | | | | 1225 | | | | | 1230 | | | | | | |
| Ser | Ser | Ala | Gln | Ser | Arg | Ser | Gly | Gln | Pro | Gln | Lys | Ala | Ala | Thr | Cys | |
| 1235 | | | | | 1240 | | | | | 1245 | | | | | | |
| Lys | Val | Ser | Ser | Ile | Asn | Gln | Glu | Thr | Ile | Gln | Thr | Tyr | Cys | Val | Glu | |
| 1250 | | | | | 1255 | | | | | 1260 | | | | | | |
| Asp | Thr | Pro | Ile | Cys | Phe | Ser | Arg | Cys | Ser | Ser | Leu | Ser | Ser | Leu | Ser | |
| 1265 | | | | | 1270 | | | | | 1275 | | | | | 1280 | |
| Ser | Ala | Glu | Asp | Glu | Ile | Gly | Cys | Asn | Gln | Thr | Thr | Gln | Glu | Ala | Asp | |
| 1285 | | | | | 1290 | | | | | 1295 | | | | | | |
| Ser | Ala | Asn | Thr | Leu | Gln | Ile | Ala | Glu | Ile | Lys | Glu | Lys | Ile | Gly | Thr | |
| 1300 | | | | | 1305 | | | | | 1310 | | | | | | |
| Arg | Ser | Ala | Glu | Asp | Pro | Val | Ser | Glu | Val | Pro | Ala | Val | Ser | Gln | His | |
| 1315 | | | | | 1320 | | | | | 1325 | | | | | | |
| Pro | Arg | Thr | Lys | Ser | Ser | Arg | Leu | Gln | Gly | Ser | Ser | Leu | Ser | Ser | Glu | |

| | | |
|---|---|----------------|
| 1330 | 1335 | 1340 |
| Ser Ala Arg His Lys | Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro | |
| 1345 | 1350 | 1355 1360 |
| Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val | | |
| | 1365 | 1370 1375 |
| Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu | | |
| | 1380 | 1385 1390 |
| Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro | | |
| | 1395 | 1400 1405 |
| Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp | | |
| | 1410 | 1415 1420 |
| Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro | | |
| | 1425 | 1430 1435 1440 |
| Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala | | |
| | 1445 | 1450 1455 |
| Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn | | |
| | 1460 | 1465 1470 |
| Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu | | |
| | 1475 | 1480 1485 |
| His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser | | |
| | 1490 | 1495 1500 |
| Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu | | |
| | 1505 | 1510 1515 1520 |
| Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr | | |
| | 1525 | 1530 1535 |
| Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala | | |
| | 1540 | 1545 1550 |
| Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp | | |
| | 1555 | 1560 1565 |
| Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr | | |
| | 1570 | 1575 1580 |
| Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu | | |
| | 1585 | 1590 1595 1600 |
| Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu | | |

| | | | | | | | | | | | | | | | | | |
|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|-----|--|--|
| 1605 | | | | | | 1610 | | | | | | 1615 | | | | | |
| Leu | Pro | Ser | Gln | Asn | Arg | Leu | Gln | Pro | Gln | Lys | His | Val | Ser | Phe | Thr | | |
| | | | 1620 | | | | | | 1625 | | | 1630 | | | | | |
| Pro | Gly | Asp | Asp | Met | Pro | Arg | Val | Tyr | Cys | Val | Glu | Gly | Thr | Pro | Ile | | |
| | | | 1635 | | | | | | 1640 | | | 1645 | | | | | |
| Asn | Phe | Ser | Thr | Ala | Thr | Ser | Leu | Ser | Asp | Leu | Thr | Ile | Glu | Ser | Pro | | |
| | | | 1650 | | | | | | 1655 | | | 1660 | | | | | |
| Pro | Asn | Glu | Leu | Ala | Ala | Gly | Glu | Gly | Val | Arg | Gly | Gly | Ala | Gln | Ser | | |
| | | | 1665 | | | | | | 1670 | | | 1675 | | | | | |
| Gly | Glu | Phe | Glu | Lys | Arg | Asp | Thr | Ile | Pro | Thr | Glu | Gly | Arg | Ser | Thr | | |
| | | | 1685 | | | | | | 1690 | | | 1695 | | | | | |
| Asp | Glu | Ala | Gln | Gly | Gly | Lys | Thr | Ser | Ser | Val | Thr | Ile | Pro | Glu | Leu | | |
| | | | 1700 | | | | | | 1705 | | | 1710 | | | | | |
| Asp | Asp | Asn | Lys | Ala | Glu | Glu | Gly | Asp | Ile | Leu | Ala | Glu | Cys | Ile | Asn | | |
| | | | 1715 | | | | | | 1720 | | | 1725 | | | | | |
| Ser | Ala | Met | Pro | Lys | Gly | Lys | Ser | His | Lys | Pro | Phe | Arg | Val | Lys | Lys | | |
| | | | 1730 | | | | | | 1735 | | | 1740 | | | | | |
| Ile | Met | Asp | Gln | Val | Gln | Gln | Ala | Ser | Ala | Ser | Ser | Ser | Ala | Pro | Asn | | |
| | | | 1745 | | | | | | 1750 | | | 1755 | | | | | |
| Lys | Asn | Gln | Leu | Asp | Gly | Lys | Lys | Lys | Lys | Pro | Thr | Ser | Pro | Val | Lys | | |
| | | | 1765 | | | | | | 1770 | | | 1775 | | | | | |
| Pro | Ile | Pro | Gln | Asn | Thr | Glu | Tyr | Arg | Thr | Arg | Val | Arg | Lys | Asn | Ala | | |
| | | | 1780 | | | | | | 1785 | | | 1790 | | | | | |
| Asp | Ser | Lys | Asn | Asn | Leu | Asn | Ala | Glu | Arg | Val | Phe | Ser | Asp | Asn | Lys | | |
| | | | 1795 | | | | | | 1800 | | | 1805 | | | | | |
| Asp | Ser | Lys | Lys | Gln | Asn | Leu | Lys | Asn | Asn | Ser | Lys | Asp | Phe | Asn | Asp | | |
| | | | 1810 | | | | | | 1815 | | | 1820 | | | | | |
| Lys | Leu | Pro | Asn | Asn | Glu | Asp | Arg | Val | Arg | Gly | Ser | Phe | Ala | Phe | Asp | | |
| | | | 1825 | | | | | | 1830 | | | 1835 | | | | | |
| Ser | Pro | His | His | Tyr | Thr | Pro | Ile | Glu | Gly | Thr | Pro | Tyr | Cys | Phe | Ser | | |
| | | | 1845 | | | | | | 1850 | | | 1855 | | | | | |
| Arg | Asn | Asp | Ser | Leu | Ser | Ser | Leu | Asp | Phe | Asp | Asp | Asp | Asp | Val | Asp | | |
| | | | 1860 | | | | | | 1865 | | | 1870 | | | | | |
| Leu | Ser | Arg | Glu | Lys | Ala | Glu | Leu | Arg | Lys | Ala | Lys | Glu | Asn | Lys | Glu | | |

| | | |
|---|-------------------------|-----------------|
| 1875 | 1880 | 1885 |
| Ser Glu Ala Lys Val Thr | Ser His Thr Glu Leu Thr | Ser Asn Gln Gln |
| 1890 | 1895 | 1900 |
| Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly | | |
| 1905 | 1910 | 1915 1920 |
| Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser | | |
| | 1925 | 1930 1935 |
| Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn | | |
| | 1940 | 1945 1950 |
| Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu | | |
| | 1955 | 1960 |
| Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu | | |
| | 1970 | 1975 1980 |
| Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys | | |
| | 1985 | 1990 1995 2000 |
| Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr | | |
| | 2005 | 2010 2015 |
| Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp | | |
| | 2020 | 2025 2030 |
| Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys | | |
| | 2035 | 2040 2045 |
| Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro | | |
| | 2050 | 2055 2060 |
| Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys | | |
| | 2065 | 2070 2075 2080 |
| Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu | | |
| | 2085 | 2090 2095 |
| Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser | | |
| | 2100 | 2105 2110 |
| Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser | | |
| | 2115 | 2120 2125 |
| Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly | | |
| | 2130 | 2135 2140 |
| Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser | | |

| | | | |
|---|------|------|------|
| 2145 | 2150 | 2155 | 2160 |
| Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu | | | |
| | 2165 | 2170 | 2175 |
| Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys | | | |
| | 2180 | 2185 | 2190 |
| Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile | | | |
| | 2195 | 2200 | 2205 |
| Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser | | | |
| | 2210 | 2215 | 2220 |
| Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser | | | |
| | 2225 | 2230 | 2235 |
| Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala | | | |
| | 2245 | 2250 | 2255 |
| Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly | | | |
| | 2260 | 2265 | 2270 |
| Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr | | | |
| | 2275 | 2280 | 2285 |
| Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg | | | |
| | 2290 | 2295 | 2300 |
| Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile | | | |
| | 2305 | 2310 | 2315 |
| Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser | | | |
| | 2325 | 2330 | 2335 |
| Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr | | | |
| | 2340 | 2345 | 2350 |
| Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro | | | |
| | 2355 | 2360 | 2365 |
| Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser | | | |
| | 2370 | 2375 | 2380 |
| Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu | | | |
| | 2385 | 2390 | 2395 |
| Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser | | | |
| | 2405 | 2410 | 2415 |
| Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu | | | |

| | | |
|---|------|------|
| 2420 | 2425 | 2430 |
| Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser | | |
| 2435 | 2440 | 2445 |
| Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu | | |
| 2450 | 2455 | 2460 |
| Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr | | |
| 2465 | 2470 | 2475 |
| Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser | | |
| 2485 | 2490 | 2495 |
| Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro | | |
| 2500 | 2505 | 2510 |
| Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala | | |
| 2515 | 2520 | 2525 |
| Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly | | |
| 2530 | 2535 | 2540 |
| Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val | | |
| 2545 | 2550 | 2555 |
| Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser | | |
| 2565 | 2570 | 2575 |
| Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn | | |
| 2580 | 2585 | 2590 |
| Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys | | |
| 2595 | 2600 | 2605 |
| Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser | | |
| 2610 | 2615 | 2620 |
| Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys | | |
| 2625 | 2630 | 2635 |
| Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val | | |
| 2645 | 2650 | 2655 |
| Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg | | |
| 2660 | 2665 | 2670 |
| Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys | | |
| 2675 | 2680 | 2685 |
| Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn | | |

| | | | | | | | | | | | | | | Pro | Leu | Thr | Glu |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | | | | | | | | | | | | 175 | | | |
| Asn | Phe | Ser | Leu | Gln | Thr | Asp | Met | Thr | Arg | Arg | Gln | Leu | Glu | Tyr | Glu | | |
| 180 | | | | | | | 185 | | | | 190 | | | | | | |
| Ala | Arg | Gln | Ile | Arg | Val | Ala | Met | Glu | Glu | Gln | Leu | Gly | Thr | Cys | Gln | | |
| 195 | | | | | | | 200 | | | | 205 | | | | | | |
| Asp | Met | Glu | Lys | Arg | Ala | Gln | Arg | Arg | Ile | Ala | Arg | Ile | Gln | Gln | Ile | | |
| 210 | | | | | | | 215 | | | | 220 | | | | | | |
| Glu | Lys | Asp | Ile | Leu | Arg | Ile | Arg | Gln | Leu | Leu | Gln | Ser | Gln | Ala | Thr | | |
| 225 | | | | | | | 230 | | | | 235 | | | | 240 | | |
| Glu | Ala | Glu | Arg | Ser | Ser | Gln | Asn | Lys | His | Glu | Thr | Gly | Ser | His | Asp | | |
| 245 | | | | | | | 250 | | | | 255 | | | | | | |
| Ala | Glu | Arg | Gln | Asn | Glu | Gly | Gln | Gly | Val | Gly | Glu | Ile | Asn | Met | Ala | | |
| 260 | | | | | | | 265 | | | | 270 | | | | | | |
| Thr | Ser | Gly | Asn | Gly | Gln | Gly | Ser | Thr | Thr | Arg | Met | Asp | His | Glu | Thr | | |
| 275 | | | | | | | 280 | | | | 285 | | | | | | |
| Ala | Ser | Val | Leu | Ser | Ser | Ser | Ser | Thr | His | Ser | Ala | Pro | Arg | Arg | Leu | | |
| 290 | | | | | | | 295 | | | | 300 | | | | | | |
| Thr | Ser | His | Leu | Gly | Thr | Lys | Val | Glu | Met | Val | Tyr | Ser | Leu | Leu | Ser | | |
| 305 | | | | | | | 310 | | | | 315 | | | | 320 | | |
| Met | Leu | Gly | Thr | His | Asp | Lys | Asp | Asp | Met | Ser | Arg | Thr | Leu | Leu | Ala | | |
| 325 | | | | | | | 330 | | | | 335 | | | | | | |

| | | | |
|---|-----|-----|-----|
| Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys | 340 | 345 | 350 |
| Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val | 355 | 360 | 365 |
| Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser | 370 | 375 | 380 |
| Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly | 385 | 390 | 395 |
| Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr | 405 | 410 | 415 |
| Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp | 420 | 425 | 430 |
| Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro | 435 | 440 | 445 |
| Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His | 450 | 455 | 460 |
| Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln | 465 | 470 | 475 |
| Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr | 485 | 490 | 495 |
| Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp | 500 | 505 | 510 |
| Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala | 515 | 520 | 525 |
| Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile | 530 | 535 | 540 |
| Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys | 545 | 550 | 555 |
| Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala | 565 | 570 | 575 |
| Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu | 580 | 585 | 590 |
| Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala | 595 | 600 | 605 |
| Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser | 610 | 615 | 620 |
| Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg | 625 | 630 | 635 |
| Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu | 645 | 650 | 655 |
| Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His | 660 | 665 | 670 |
| Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser | 675 | 680 | 685 |
| Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val | 690 | 695 | 700 |
| Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met | 705 | 710 | 715 |
| Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys | 725 | 730 | 735 |
| Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu | | | |

| | | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|
| 740 | | | | | 745 | | | | | 750 | | | | | | |
| His | Val | Arg | Lys | Gln | Lys | Ala | Leu | Glu | Ala | Glu | Leu | Asp | Ala | Gln | His | |
| 755 | | | | | 760 | | | | | 765 | | | | | | |
| Leu | Ser | Glu | Thr | Phe | Asp | Asn | Ile | Asp | Asn | Leu | Ser | Pro | Lys | Ala | Ser | |
| 770 | | | | | 775 | | | | | 780 | | | | | | |
| His | Arg | Ser | Lys | Gln | Arg | His | Lys | Gln | Ser | Leu | Tyr | Gly | Asp | Tyr | Val | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Phe | Asp | Thr | Asn | Arg | His | Asp | Asp | Asn | Arg | Ser | Asp | Asn | Phe | Asn | Thr | |
| 805 | | | | | 810 | | | | | 815 | | | | | | |
| Gly | Asn | Met | Thr | Val | Leu | Ser | Pro | Tyr | Leu | Asn | Thr | Thr | Val | Leu | Pro | |
| 820 | | | | | 825 | | | | | 830 | | | | | | |
| Ser | Ser | Ser | Ser | Ser | Arg | Gly | Ser | Leu | Asp | Ser | Ser | Arg | Ser | Glu | Lys | |
| 835 | | | | | 840 | | | | | 845 | | | | | | |
| Asp | Arg | Ser | Leu | Glu | Arg | Glu | Arg | Gly | Ile | Gly | Leu | Gly | Asn | Tyr | His | |
| 850 | | | | | 855 | | | | | 860 | | | | | | |
| Pro | Ala | Thr | Glu | Asn | Pro | Gly | Thr | Ser | Ser | Lys | Arg | Gly | Leu | Gln | Ile | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |
| Ser | Thr | Thr | Ala | Ala | Gln | Ile | Ala | Lys | Val | Met | Glu | Glu | Val | Ser | Ala | |
| 885 | | | | | 890 | | | | | 895 | | | | | | |
| Ile | His | Thr | Ser | Gln | Glu | Asp | Arg | Ser | Ser | Gly | Ser | Thr | Thr | Glu | Leu | |
| 900 | | | | | 905 | | | | | 910 | | | | | | |
| His | Cys | Val | Thr | Asp | Glu | Arg | Asn | Ala | Leu | Arg | Arg | Ser | Ser | Ala | Ala | |
| 915 | | | | | 920 | | | | | 925 | | | | | | |
| His | Thr | His | Ser | Asn | Thr | Tyr | Asn | Phe | Thr | Lys | Ser | Glu | Asn | Ser | Asn | |
| 930 | | | | | 935 | | | | | 940 | | | | | | |
| Arg | Thr | Cys | Ser | Met | Pro | Tyr | Ala | Lys | Leu | Glu | Tyr | Lys | Arg | Ser | Ser | |
| 945 | | | | | 950 | | | | | 955 | | | | | 960 | |
| Asn | Asp | Ser | Leu | Asn | Ser | Val | Ser | Ser | Ser | Asp | Gly | Tyr | Gly | Lys | Arg | |
| 965 | | | | | 970 | | | | | 975 | | | | | | |
| Gly | Gln | Met | Lys | Pro | Ser | Ile | Glu | Ser | Tyr | Ser | Glu | Asp | Asp | Glu | Ser | |
| 980 | | | | | 985 | | | | | 990 | | | | | | |
| Lys | Phe | Cys | Ser | Tyr | Gly | Gln | Tyr | Pro | Ala | Asp | Leu | Ala | His | Lys | Ile | |
| 995 | | | | | 1000 | | | | | 1005 | | | | | | |
| His | Ser | Ala | Asn | His | Met | Asp | Asp | Asn | Asp | Gly | Glu | Leu | Asp | Thr | Pro | |
| 1010 | | | | | 1015 | | | | | 1020 | | | | | | |
| Ile | Asn | Tyr | Ser | Leu | Lys | Tyr | Ser | Asp | Glu | Gln | Leu | Asn | Ser | Gly | Arg | |
| 1025 | | | | | 1030 | | | | | 1035 | | | | | 1040 | |
| Gln | Ser | Pro | Ser | Gln | Asn | Glu | Arg | Trp | Ala | Arg | Pro | Lys | His | Ile | Ile | |
| 1045 | | | | | 1050 | | | | | 1055 | | | | | | |
| Glu | Asp | Glu | Ile | Lys | Gln | Ser | Glu | Gln | Arg | Gln | Ser | Arg | Asn | Gln | Ser | |
| 1060 | | | | | 1065 | | | | | 1070 | | | | | | |
| Thr | Thr | Tyr | Pro | Val | Tyr | Thr | Glu | Ser | Thr | Asp | Asp | Lys | His | Leu | Lys | |
| 1075 | | | | | 1080 | | | | | 1085 | | | | | | |
| Phe | Gln | Pro | His | Phe | Gly | Gln | Gln | Glu | Cys | Val | Ser | Pro | Tyr | Arg | Ser | |
| 1090 | | | | | 1095 | | | | | 1100 | | | | | | |
| Arg | Gly | Ala | Asn | Gly | Ser | Glu | Thr | Asn | Arg | Val | Gly | Ser | Asn | His | Gly | |
| 1105 | | | | | 1110 | | | | | 1115 | | | | | 1120 | |
| Ile | Asn | Gln | Asn | Val | Ser | Gln | Ser | Leu | Cys | Gln | Glu | Asp | Asp | Tyr | Glu | |
| 1125 | | | | | 1130 | | | | | 1135 | | | | | | |
| Asp | Asp | Lys | Pro | Thr | Asn | Tyr | Ser | Glu | Arg | Tyr | Ser | Glu | Glu | Glu | Gln | |
| 1140 | | | | | 1145 | | | | | 1150 | | | | | | |

| | | | |
|---|------|------|------|
| His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu | | | |
| 1155 | 1160 | 1165 | |
| Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala | | | |
| 1170 | 1175 | 1180 | |
| Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser | | | |
| 1185 | 1190 | 1195 | 1200 |
| Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu | | | |
| 1205 | 1210 | 1215 | |
| Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His | | | |
| 1220 | 1225 | 1230 | |
| Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr | | | |
| 1235 | 1240 | 1245 | |
| Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val | | | |
| 1250 | 1255 | 1260 | |
| Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu | | | |
| 1265 | 1270 | 1275 | 1280 |
| Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala | | | |
| 1285 | 1290 | 1295 | |
| Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly | | | |
| 1300 | 1305 | 1310 | |
| Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln | | | |
| 1315 | 1320 | 1325 | |
| His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser | | | |
| 1330 | 1335 | 1340 | |
| Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser | | | |
| 1345 | 1350 | 1355 | 1360 |
| Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr | | | |
| 1365 | 1370 | 1375 | |
| Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser | | | |
| 1380 | 1385 | 1390 | |
| Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu | | | |
| 1395 | 1400 | 1405 | |
| Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro | | | |
| 1410 | 1415 | 1420 | |
| Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro | | | |
| 1425 | 1430 | 1435 | 1440 |
| Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys | | | |
| 1445 | 1450 | 1455 | |
| Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val | | | |
| 1460 | 1465 | 1470 | |
| Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu | | | |
| 1475 | 1480 | 1485 | |
| Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser | | | |
| 1490 | 1495 | 1500 | |
| Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val | | | |
| 1505 | 1510 | 1515 | 1520 |
| Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu | | | |
| 1525 | 1530 | 1535 | |
| Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu | | | |
| 1540 | 1545 | 1550 | |
| Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp | | | |

| | | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|
| 1555 | | | | | 1560 | | | | | 1565 | | | | | | |
| Asp | Asp | Asp | Ile | Glu | Ile | Leu | Glu | Glu | Cys | Ile | Ile | Ser | Ala | Met | Pro | |
| 1570 | | | | | 1575 | | | | | 1580 | | | | | | |
| Thr | Lys | Ser | Ser | Arg | Lys | Ala | Lys | Lys | Pro | Ala | Gln | Thr | Ala | Ser | Lys | |
| 1585 | | | | | 1590 | | | | | 1595 | | | | | 1600 | |
| Leu | Pro | Pro | Pro | Val | Ala | Arg | Lys | Pro | Ser | Gln | Leu | Pro | Val | Tyr | Lys | |
| 1605 | | | | | 1610 | | | | | 1615 | | | | | | |
| Leu | Leu | Pro | Ser | Gln | Asn | Arg | Leu | Gln | Pro | Gln | Lys | His | Val | Ser | Phe | |
| 1620 | | | | | 1625 | | | | | 1630 | | | | | | |
| Thr | Pro | Gly | Asp | Asp | Met | Pro | Arg | Val | Tyr | Cys | Val | Glu | Gly | Thr | Pro | |
| 1635 | | | | | 1640 | | | | | 1645 | | | | | | |
| Ile | Asn | Phe | Ser | Thr | Ala | Thr | Ser | Leu | Ser | Asp | Leu | Thr | Ile | Glu | Ser | |
| 1650 | | | | | 1655 | | | | | 1660 | | | | | | |
| Pro | Pro | Asn | Glu | Leu | Ala | Ala | Gly | Glu | Gly | Val | Arg | Gly | Gly | Ala | Gln | |
| 1665 | | | | | 1670 | | | | | 1675 | | | | | 1680 | |
| Ser | Gly | Glu | Phe | Glu | Lys | Arg | Asp | Thr | Ile | Pro | Thr | Glu | Gly | Arg | Ser | |
| 1685 | | | | | 1690 | | | | | 1695 | | | | | | |
| Thr | Asp | Glu | Ala | Gln | Gly | Gly | Lys | Thr | Ser | Ser | Val | Thr | Ile | Pro | Glu | |
| 1700 | | | | | 1705 | | | | | 1710 | | | | | | |
| Leu | Asp | Asp | Asn | Lys | Ala | Glu | Glu | Gly | Asp | Ile | Leu | Ala | Glu | Cys | Ile | |
| 1715 | | | | | 1720 | | | | | 1725 | | | | | | |
| Asn | Ser | Ala | Met | Pro | Lys | Gly | Lys | Ser | His | Lys | Pro | Phe | Arg | Val | Lys | |
| 1730 | | | | | 1735 | | | | | 1740 | | | | | | |
| Lys | Ile | Met | Asp | Gln | Val | Gln | Gln | Ala | Ser | Ala | Ser | Ser | Ser | Ala | Pro | |
| 1745 | | | | | 1750 | | | | | 1755 | | | | | 1760 | |
| Asn | Lys | Asn | Gln | Leu | Asp | Gly | Lys | Lys | Lys | Lys | Pro | Thr | Ser | Pro | Val | |
| 1765 | | | | | 1770 | | | | | 1775 | | | | | | |
| Lys | Pro | Ile | Pro | Gln | Asn | Thr | Glu | Tyr | Arg | Thr | Arg | Val | Arg | Lys | Asn | |
| 1780 | | | | | 1785 | | | | | 1790 | | | | | | |
| Ala | Asp | Ser | Lys | Asn | Asn | Leu | Asn | Ala | Glu | Arg | Val | Phe | Ser | Asp | Asn | |
| 1795 | | | | | 1800 | | | | | 1805 | | | | | | |
| Lys | Asp | Ser | Lys | Lys | Gln | Asn | Leu | Lys | Asn | Asn | Ser | Lys | Asp | Phe | Asn | |
| 1810 | | | | | 1815 | | | | | 1820 | | | | | | |
| Asp | Lys | Leu | Pro | Asn | Asn | Glu | Asp | Arg | Val | Arg | Gly | Ser | Phe | Ala | Phe | |
| 1825 | | | | | 1830 | | | | | 1835 | | | | | 1840 | |
| Asp | Ser | Pro | His | His | Tyr | Thr | Pro | Ile | Glu | Gly | Thr | Pro | Tyr | Cys | Phe | |
| 1845 | | | | | 1850 | | | | | 1855 | | | | | | |
| Ser | Arg | Asn | Asp | Ser | Leu | Ser | Ser | Leu | Asp | Phe | Asp | Asp | Asp | Asp | Val | |
| 1860 | | | | | 1865 | | | | | 1870 | | | | | | |
| Asp | Leu | Ser | Arg | Glu | Lys | Ala | Glu | Leu | Arg | Lys | Ala | Lys | Glu | Asn | Lys | |
| 1875 | | | | | 1880 | | | | | 1885 | | | | | | |
| Glu | Ser | Glu | Ala | Lys | Val | Thr | Ser | His | Thr | Glu | Leu | Thr | Ser | Asn | Gln | |
| 1890 | | | | | 1895 | | | | | 1900 | | | | | | |
| Gln | Ser | Ala | Asn | Lys | Thr | Gln | Ala | Ile | Ala | Lys | Gln | Pro | Ile | Asn | Arg | |
| 1905 | | | | | 1910 | | | | | 1915 | | | | | 1920 | |
| Gly | Gln | Pro | Lys | Pro | Ile | Leu | Gln | Lys | Gln | Ser | Thr | Phe | Pro | Gln | Ser | |
| 1925 | | | | | 1930 | | | | | 1935 | | | | | | |
| Ser | Lys | Asp | Ile | Pro | Asp | Arg | Gly | Ala | Ala | Thr | Asp | Glu | Lys | Leu | Gln | |
| 1940 | | | | | 1945 | | | | | 1950 | | | | | | |
| Asn | Phe | Ala | Ile | Glu | Asn | Thr | Pro | Val | Cys | Phe | Ser | His | Asn | Ser | Ser | |
| 1955 | | | | | 1960 | | | | | 1965 | | | | | | |

| | | | |
|---|------|------|------|
| Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn | | | |
| 1970 | 1975 | 1980 | |
| Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser | | | |
| 1985 | 1990 | 1995 | 2000 |
| Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp | | | |
| 2005 | 2010 | 2015 | |
| Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile | | | |
| 2020 | 2025 | 2030 | |
| Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro | | | |
| 2035 | 2040 | 2045 | |
| Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser | | | |
| 2050 | 2055 | 2060 | |
| Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu | | | |
| 2065 | 2070 | 2075 | 2080 |
| Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser | | | |
| 2085 | 2090 | 2095 | |
| Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val | | | |
| 2100 | 2105 | 2110 | |
| Ser Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala | | | |
| 2115 | 2120 | 2125 | |
| Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu | | | |
| 2130 | 2135 | 2140 | |
| Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr | | | |
| 2145 | 2150 | 2155 | 2160 |
| Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu | | | |
| 2165 | 2170 | 2175 | |
| Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys | | | |
| 2180 | 2185 | 2190 | |
| Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu | | | |
| 2195 | 2200 | 2205 | |
| Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile | | | |
| 2210 | 2215 | 2220 | |
| Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser | | | |
| 2225 | 2230 | 2235 | 2240 |
| Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro | | | |
| 2245 | 2250 | 2255 | |
| Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg | | | |
| 2260 | 2265 | 2270 | |
| Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln | | | |
| 2275 | 2280 | 2285 | |
| Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser | | | |
| 2290 | 2295 | 2300 | |
| Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro | | | |
| 2305 | 2310 | 2315 | 2320 |
| Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile | | | |
| 2325 | 2330 | 2335 | |
| Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser | | | |
| 2340 | 2345 | 2350 | |
| Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser | | | |
| 2355 | 2360 | 2365 | |
| Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu | | | |

| | | |
|---|---|-----------|
| 2370 | 2375 | 2380 |
| Ser Lys Asn Ala | Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly | |
| 2385 | 2390 | 2395 2400 |
| Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu | | |
| 2405 | 2410 | 2415 |
| Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser | | |
| 2420 | 2425 | 2430 |
| Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro | | |
| 2435 | 2440 | 2445 |
| Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser | | |
| 2450 | 2455 | 2460 |
| Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln | | |
| 2465 | 2470 | 2475 2480 |
| Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His | | |
| 2485 | 2490 | 2495 |
| Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser | | |
| 2500 | 2505 | 2510 |
| Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile | | |
| 2515 | 2520 | 2525 |
| Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser | | |
| 2530 | 2535 | 2540 |
| Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg | | |
| 2545 | 2550 | 2555 2560 |
| Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala | | |
| 2565 | 2570 | 2575 |
| Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val | | |
| 2580 | 2585 | 2590 |
| Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala | | |
| 2595 | 2600 | 2605 |
| Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn | | |
| 2610 | 2615 | 2620 |
| Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser | | |
| 2625 | 2630 | 2635 2640 |
| Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp | | |
| 2645 | 2650 | 2655 |
| Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly | | |
| 2660 | 2665 | 2670 |
| Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu | | |
| 2675 | 2680 | 2685 |
| Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln | | |
| 2690 | 2695 | 2700 |
| Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn | | |
| 2705 | 2710 | 2715 2720 |
| Arg Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr | | |
| 2725 | 2730 | 2735 |
| Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn | | |
| 2740 | 2745 | 2750 |
| Glu Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser | | |
| 2755 | 2760 | 2765 |
| Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe | | |
| 2770 | 2775 | 2780 |

| | | | | | | | | | | | | | | | |
|------|-----|------|------|-----|------|-----|------|------|------|------|-----|-----|------|------|------|
| Asn | Tyr | Asn | Pro | Ser | Pro | Arg | Lys | Ser | Ser | Ala | Asp | Ser | Thr | Ser | Ala |
| 2785 | | | | | 2790 | | | | | 2795 | | | | | 2800 |
| Arg | Pro | Ser | Gln | Ile | Pro | Thr | Pro | Val | Asn | Asn | Asn | Thr | Lys | Lys | Arg |
| | | | 2805 | | | | | | 2810 | | | | | 2815 | |
| Asp | Ser | Lys | Thr | Asp | Ser | Thr | Glu | Ser | Ser | Gly | Thr | Gln | Ser | Pro | Lys |
| | | | 2820 | | | | | 2825 | | | | | 2830 | | |
| Arg | His | Ser | Gly | Ser | Tyr | Leu | Val | Thr | Ser | Val | | | | | |
| | | 2835 | | | | | 2840 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ral2(yeast)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Gly | Ala | Lys | Gly | Leu | Gln | Leu | Arg | Ala | Leu | Arg | Arg | Ile | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Arg | Ile | Glu | Gln | Gly | Gly | Thr | Ala | Ile | Ser | Pro | Thr | Ser | Pro | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: m3(mAChR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu
1 5 10 15

Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MCC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu
1 5 10 15

Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met
 20 25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATTTT

40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTAGAATTT CATGTTAATA TATTGTGTTT TTTTAAACAG

40

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTAAGATTTTA AAAAGGTGTT TTAAAATAAT TTTTAAAGCT

40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCAATTGT TGTATAAAAA CTTGTTTCTA TTTTATTTAG

40

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAACCTTTC TTCATATAGT AACATTGCC TTGTGTACTC

40

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNNGTCCCTT TTTTAAAAA AAAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTTGA AACTTTAATA

40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTTAG

40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTTTCTAAG TGATAAAACA GYGAAGAGCT

40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAACA TAACTAATTA GGTTCCTTGT TTTATTTTAG

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTTT GTTTGTGGGT ATAAAAATAG

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTGT CATGTACTGA TGTAACTCC ATCTTAACAG

40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAT TATTTTATCA TATTTTAA AATTATTTAA

40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT

60

TTAG

64

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAACAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTTGCTA AG

52

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATATTAAA GTCGTAATTT TGTTCCTAAA CTCATTTGGC CCACAG

46

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTATGTTCTC TATAGTGAC ATCGTAGTGC ATGTTTCAAA

40

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCATTGCT CTTCAAATAA CAAAGCATTA TGGTTTATGT TGATTTTATT TTTCAG

56

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTAAGACAAA AATGTTTTTTT AATGACATAG ACAATTACTG GTG

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCTTTTCC TCTTGCCCTT TTAAATTAG

40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA 44

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTTAATGATC CTCTATTCTG TATTTAATTT ACAG 54

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTTA GAATTCACCT TGTTTTTCTT TTTTCTCTTT TTCTTTGAGG CAGGGTCTCA 60

CTCTG 65

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTTCC AG

52

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTTGA AAACATTTAG TACTATAATA TGAATTTTCAT GT

42

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAACCTNAA TTAGATGACC CATATTCAGA AACTTACTAG

40

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTTATAT TACTTTTAAA GTACAGAATT CATACTCTCA AAAA

54

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTTGTG ATCTCTTGAT TTTTATTTC A G

41

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGCCTG CCGCTCTC

18

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGCGG CTCCCGTG

18

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCCTAC TTCTTCTATA CAG

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTCTTTTT C

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTTCTGA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTAGGCA CAAAGCTTGC AA

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCGGCTCCT GGGTTGTTG

19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCTTCCT TTCTGAGGAC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTCTCCTG CCTCTTACTG C

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCCTC

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

22

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTTCT TTTG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTTAGAACCT TTTTGTGTT GTG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT AACTAAGCC TAAC

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CATGTCTCTT ACAGTAGTAC CA

22

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAAAAATGGA TAAACTACAA TTAAAAG

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGTCTTG AAGT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATTT GAG

23

- (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAATT TCCC

24

- (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

23

- (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATAGGTCATT GCTTCTTGCT GAT

23

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGAATTTTAA TGGATTACCT AGGT

24

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTTTTTTGC TTTTACTGAT TAACG

25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGTAATTCAT TTTATTCCTA ATA[G]CCTC

27

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

24

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATTT TTATACCCAC AAAC

24

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTT TGC

23

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAC CATC

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCATGGCAT TAGTGACCAG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGTCGTAATT TTGTTTCTAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGAAGGACTC GGATTTTCAC[G]C C

21

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCATTCACTC ACAGCCTGAT GAC

23

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTTTGAAAC ATGCACTACG AT

22

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AAACATCATT GCTCTTCAAA TAAC

24

- (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TACCATGATT TAAAAATCCA CCAG

24

- (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATGATTGTC TTTTTCCTCT TGC

23

- (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGAGCTATC TTAAGAAATA CATG

24

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTC TGTAT

25

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAG

24

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

22

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

22

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGTGAGAG TA

22

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTACTGCAT ACACATTGTG AC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTGTTCCTAACATG AAG

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCCACAG GTAATACTCC C

21

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGGTAC G

21

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGAAGGATCCCTTGTGCAGTGTGGA

24

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

GACAGGATCCTGAAGCTGAGTTTG

24

- (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAGTGCTGAAGAG

18

- (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGAATAATTAGGTCTCAA

19

- (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTAAGAGAGAACAA

21

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATGGCAAGCTTGAGCCAG

19

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTTCCAGCAGTGTACAG

18

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGAGATTTGCTCCTGA

102

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AGTACAAGGA TGCCAATATT ATG

23

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACTTCTATCT TTTTCAGAAC GAG

23

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:105:

ATTTGAATAC TACAGTGTTA CCC

23

(2) INFORMATION FOR SEO ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:106:

CTTGTTATTCT AATTTGGCAT AAGG

24

(2) INFORMATION FOR SEO ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:107:

CTGCCCATAC ACATTCAAAC AC

22

(2) INFORMATION FOR SEO ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:108:

TGTTTGCCTC TTGCCCATCT T 21

(2) INFORMATION FOR SEO ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:109:

AGTCTTAAAT ATTCAGATGA GCAG 24

(2) INFORMATION FOR SEO ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:110:

GTTTCTCTTC ATTATATTTT ATGCTA 26

(2) INFORMATION FOR SEO ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:111:
AAGCCTACCA ATTATAGTGA ACG 23

(2) INFORMATION FOR SEO ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:112:
AGCTGATGAC AAAGATGATA ATC 23

(2) INFORMATION FOR SEO ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:113:
AAGAAACAAT ACAGACTTAT TGTG 24

(2) INFORMATION FOR SEO ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGAGTGGGG TCTCCTGAAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATCTCCCTCC AAAAGTGGTG C

21

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TCCATCTGGA GTACTTTCTG TG

22

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGTAAATGCT GCAGTTCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCGTGGCATA TCATCCCCC

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCAGACTGC TTCAAATTA CC

22

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAGCCTCATC TGTAATTCTG C

21

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CCCTCCAAAT GAGTTAGCTG C

21

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TTGTGGTATA GGTTTTACTG GTG

23

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACCCAACAAA AATCAGTTAG ATG

23

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GTGGCTGGTA ACTTTAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGATGTTGA CCTTTCCAGG G

21

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATTGTGTAAC TTTTCATCAG TTGC

24

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AAAGACATAC CAGACAGAGG G

21

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTTTTTGGC ATTGCGGAGC T

21

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AAGATGACCT GTTGCAGGAA TG

22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATCAGACC AAGCTTGTCT AGAT

24

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CAATAGTAAG TAGTTTACAT CAAG

24

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AAACAGGACT TGTACTGTAG GA

22

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CAGCCCCTTC AAGCAAACAT C

21

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAGGACTTAT TCCATTTCTA CC

22

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CAGTCTCCTG GCCGAAACTC

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:139:

22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

24

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(A) Homo sapiens
(xi) SEQUENCE DESCRIPTION: SEO ID NO:145:
CAGGACAAAA TAATCCTGTC CC

22

(2) INFORMATION FOR SEO ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:146:

ATTTTCTTAC TTTCATTCTT CCTC

24

(2) INFORMATION FOR SEO ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) Artificial sequence (consensus)

(xi) SEQUENCE DESCRIPTION: SEO ID NO:147:

Phe Xaa Val Glu Xaa Thr Pro Xaa Cys Phe Ser Arg Xaa Ser Ser Leu Ser Ser Leu
1 5 10 15

Ser
20

(2) INFORMATION FOR SEO ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:148:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Cys | Val | Glu | Asp | Thr | Pro | Ile | Cys | Phe | Ser | Arg | Cys | Ser | Ser | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ser | Ser | Leu | Ser | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEO ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:149:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Val | Gln | Glu | Thr | Pro | Leu | Met | Phe | Ser | Arg | Cys | Thr | Ser | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ser | Ser | Leu | Asp | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEO ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:150:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ala | Thr | Glu | Ser | Thr | Pro | Asp | Gly | Phe | Ser | Cys | Ser | Ser | Ser | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ser | Ala | Leu | Ser | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEO ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:151:

Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr Ser Leu
1 5 10 15
Ser Asp Leu Thr
20

(2) INFORMATION FOR SEO ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:152:

Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu
1 5 10 15
Ser Ser Leu Asp
20

(2) INFORMATION FOR SEO ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:153:

Phe Ala Ile Glu Asn Thr Pro Val Cys Pro Ser His Asn Ser Ser Leu
1 5 10 15
Ser Ser Leu Ser
20

(2) INFORMATION FOR SEO ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEO ID NO:154:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Val | Glu | Asp | Thr | Pro | Val | Cys | Phe | Ser | Arg | Asn | Ser | Ser | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Ser | Leu | Ser | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |